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!!SEQUENCE_LIST 1.0
(Nucleotide) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-1 check: 7546 from:

FROMIG of: /home/obryen/ree455/olig/US08836455.seq
sequence 1, application us/08836455

general information:
applicant: chatterjee, malaya
applicant: foon, kenneth a.
applicant: chatterjee, sunil k. . .

TO: geneseqn: * Sequences: 240,622 Total-length: 94,065,609 April 18, 1999 13:41

Database Release Information:

Geneseq: NA, Release 34.4, Released on 4Feb1999, Formatted on 5Feb1999.

Word-size: 15 Words: 48182 Diagonals: 1,619 Total diagonals: 396,990,246
Integral-width: 1 Alphabet: 4 List-size: 50 CPU minutes: 29.44

Sequence Seqd Diag Score Width Documentation ..

GENESON:T85149	+	0	435	1	Murine monoclonal anti-idiotypic anti
GENESON:N30165	+	18	345	1	Sequence encoding the leader, variabl
GENESON:Q46084	+	339	306	1	Sequence encoding 520C9 sfv protein.
GENESON:T36880	+	339	306	1	520C9 anti-c-erbB-2 two single chain
GENESON:V63399	+	339	306	1	520C9 sfv DNA sequence. Nucleic acid
GENESON:V21798	+	339	306	1	520C9 anti-c-erbB-2 sfv' dimeric cons
GENESON:Q46086	+	1212	287	1	Sequence encoding G-FIT. New single c
GENESON:Q97507	+	-60	262	1	light chain variable region for monoc
GENESON:Q97504	+	-60	262	1	light chain variable region for monoc
GENESON:Q97510	+	-60	261	1	light chain variable region for monoc
GENESON:T77851	+	-60	220	1	light chain variable region for monoc
GENESON:T85091	+	-60	147	1	Murine anti-human class II monoclonal
GENESON:Q30755	+	0	142	1	Mouse monoclonal antibody B9 light ch
GENESON:T87818	+	-60	128	1	PM-K3. Reconstituted human antibody
GENESON:Q36607	+	0	122	1	Antibody 362 light chain variable reg
GENESON:T51437	+	32	122	1	Anti-CD4 antibody MT 15.1 light chain
GENESON:N90672	+	15	116	1	Murine MAb SK48-E26 light chain DNA.
GENESON:Q51229	+	835	115	1	DNA sequence encoding upprocessed vari
GENESON:V20086	+	30	108	1	DNA encoding humanised anti-erbB2 spe
GENESON:V02198	+	-60	108	1	Consensus DNA sequence of the murine
GENESON:T34816	+	-60	104	1	CDNA for light chain variable region
GENESON:T34541	+	-60	104	1	Humanised anti-CD38 monoclonal antibc
GENESON:T31540	+	21	102	1	Monoclonal anti-idiotypic antibody 3H1
GENESON:T99434	+	21	102	1	3H1 light chain variable region cDNA.
GENESON:T30456	+	138	101	1	Anti-idiotypic antibody 3H1 light cha
GENESON:Q92503	+	18	100	1	HNK-20 variable kappa chain coding se
GENESON:T05311	+	0	97	1	Mouse antibody F4-7 light chain varia
GENESON:V04640	+	-60	96	1	MAb SCH94.03 light chain DNA. Monoclo
GENESON:Q14651	+	-60	96	1	Mus musculus A17 antibody light cha
GENESON:Q14801	+	30	94	1	R6-5-D6 anti-ICAM-1 light chain. New
GENESON:T04625	+	-87	94	1	Encodes murine anti-ICAM monoclonal a
GENESON:V63620	+	498	93	1	Mouse derived light chain RT3 phage a
GENESON:V63619	+	57	93	1	Nucleic acid sequence of plasmid pET-
GENESON:V63616	+	426	93	1	Nucleic acid sequence of plasmid pET-
GENESON:V63617	+	465	93	1	Nucleic acid sequence of plasmid pET-
GENESON:T94968	+	294	93	1	Nucleic acid sequence of plasmid pET-
GENESON:T94967	+	-60	93	1	R. pipiens recombinant RNase ronc fus
GENESON:T94966	+	-60	93	1	R. pipiens recombinant RNase ronc fus
GENESON:T94965	+	300	93	1	R. pipiens recombinant RNase ronc fus
GENESON:T94964	+	294	93	1	R. pipiens recombinant RNase ronc fus
GENESON:T94963	+	366	93	1	R. pipiens recombinant RNase ronc fus
GENESON:Q90431	+	-60	93	1	R. pipiens recombinant RNase ronc fus
GENESON:Q15113	+	-12	90	1	DNA encoding anti-idiotypic antibody 1
GENESON:T04625	+	-84	85	1	IL-2 chimeric antibody light chain cl
GENESON:N91657	+	-63	84	1	Mouse derived light chain RT3 phage a
GENESON:Q85387	+	31	83	1	Chimeric antibody light chain variabl
GENESON:Q46088	+	345	83	1	MAb 4197X light chain variable region
GENESON:Q30759	+	0	82	1	Sequence encoding 741 sfv-PE40. New s
GENESON:Q08608	+	60	82	1	p146-K3. Reconstituted human antibody
GENESON:Q45662	+	0	82	1	ME4 light chain V Region (mouse). Chi
					Mouse C4G1 Ig light-chain coding sequ

Not sequences containing matches at least 15 nt long

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[illegible]

186	31	7.1	46.40	7048267	Monoclonal antibody 1	7.28e-11
187	31	7.1	46.40	7048267	Primer for amplifying	7.28e-11
188	31	7.1	46.40	7048267	Mon kappa chain cont	7.28e-11
189	31	7.1	46.7	7048267	Primer for amplifying	7.28e-11
190	31	7.1	55.3	7078700	Primer to amplify CM2	7.28e-11
191	31	7.1	819.3	920381	Sequence encoding the	4.88e-10
192	31	6.9	30.11	945053	Anti-cancer monoclonal	4.88e-10
193	30	6.9	30.11	945053	Anti-cancer monoclonal	4.88e-10
194	30	6.9	30.5	918866	Anti-cancer monoclonal	4.88e-10
195	30	6.9	30.5	909039	Light chain primer 1	4.88e-10
196	30	6.9	30.21	715156	Anti-cancer monoclonal	4.88e-10
197	30	6.9	30.21	715156	3H1 V _H region 3' prim	4.88e-10
198	30	6.9	30.11	967374	Monoclonal antibody KC-4	4.88e-10
199	30	6.9	30.11	967374	Primer for amplifying	4.88e-10
200	30	6.9	30.39	788512	Primer-Chappa for mon	4.88e-10
201	30	6.9	30.5	928756	3F9 V _H -human C-kappa	4.88e-10
202	30	6.9	30.7	788418	Human antibody 5G1.1	4.88e-10
203	30	6.9	30.32	785166	Human immunoglobulin	4.88e-10
204	30	6.9	30.32	785166	Monoclonal anti-lysozyme	4.88e-10
205	30	6.9	30.32	785166	Monoclonal anti-lysozyme	4.88e-10
206	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
207	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
208	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
209	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
210	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
211	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
212	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
213	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
214	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
215	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
216	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
217	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
218	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
219	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
220	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
221	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
222	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
223	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
224	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
225	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
226	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
227	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
228	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
229	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
230	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
231	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
232	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
233	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
234	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
235	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
236	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
237	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
238	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
239	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
240	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
241	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
242	30	6.9	30.32	785166	Sequence reverse comp	4.88e-10
243	30	6.				

[illegible]

288	26	6.0	42.9	Q58202	Sequence of one of the	8.21e-07
289	26	6.0	42.9	T04655	Mouse derived rat Pn	8.21e-07
290	26	6.0	44.1	T78904	Kappa light chain PCR	8.21e-07
300	26	6.0	44.1	T78904	Kappa light chain PCR	8.21e-07
301	26	6.0	44.1	T78904	Kappa light chain PCR	8.21e-07
302	26	6.0	71.7	T15766	lambda light chain	8.21e-07
303	26	6.0	327.18	T04655	Anti-PCR antibody in	8.21e-07
304	26	6.0	331.18	T15766	lambda light chain	8.21e-07
305	26	6.0	331.18	T04655	Anti-PCR antibody in	8.21e-07
306	26	6.0	331.18	T04655	Anti-PCR antibody in	8.21e-07
307	26	6.0	38.53	T86844	Monoclonal antibody 2	8.21e-07
308	26	6.0	38.53	T86844	Monoclonal antibody 2	8.21e-07
309	26	6.0	38.53	T86844	Monoclonal antibody 2	8.21e-07
310	26	6.0	38.53	T86844	Monoclonal antibody 2	8.21e-07
311	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
312	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
313	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
314	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
315	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
316	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
317	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
318	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
319	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
320	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
321	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
322	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
323	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
324	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
325	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
326	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
327	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
328	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
329	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
330	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
331	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
332	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
333	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
334	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
335	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
336	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
337	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
338	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
339	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
340	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
341	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
342	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
343	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
344	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
345	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
346	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
347	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07
348	26	6.0	42.9	T74445	Human immunoglobulin	8.21e-07

149	24	5	5	3.3	93	V1259	Primer for mouse Igfa	2.9
150	24	5	5	3.3	77	Q4196	PER primer to amplify	2.9
151	24	5	5	50.1	17	Q4196	PER primer to amplify	2.9
152	24	5	5	50.1	17	T6829	Primer V15-455-3' for	2.9
153	24	5	5	50.1	Q6818	Diabolo primer LABS-	2.9	
154	24	5	5	3.34	34	T6510	Anti-human pAb, anti	2.9
155	24	5	5	3.34	34	T6510	Variant variable, light	2.9
156	24	5	5	3.34	34	T6510	Variant variable, heavy	2.9
157	24	5	5	3.37	16	Q6589	Human JEE receptor-3'	2.9
158	24	5	5	381.24	73550	NAB V1476	Light chain	2.9
159	24	5	5	402.2	Q12017	Sequence encoding N-g	2.9	
160	24	5	5	402.2	Q12017	Sequence encoding N-g	2.9	
161	24	5	5	408.6	Q37058	Rat immunoglobulin L	2.9	
162	24	5	5	408.11	Q54518	Rat IgL chain variable	2.9	
163	24	5	5	488.37	T68013	Coding sequence for V	2.9	
164	24	5	5	488.37	T68013	Coding sequence for V	2.9	
165	24	5	5	718.11	Q61536	DNA encoding IL6	2.9	
166	24	5	5	776.3	Q20068	Enkephalin A	2.9	
167	24	5	5	831.10	Q62357	Enkephalin A	2.9	
168	24	5	5	924.30	T66146	Sepry 4715-mgc N10 ac	2.9	
169	24	5	5	930.37	T64887	EColi-HMG1 insert	2.9	
170	24	5	5	999.30	T66145	Pr 4715-mgc insert en	2.9	
171	24	5	5	999.30	T66145	Pr 4715-mgc insert en	2.9	
172	24	5	5	999.37	T74608	EGF-purified antibody	2.9	
173	24	5	5	143.10	Q24335	EGF-purified antibody	2.9	
174	23	5	5	23.3	Q23118	Primer PAVC-BLBC for	1.7	
175	23	5	5	23.3	Q23118	Primer PAVC-BLBC for	1.7	
176	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
177	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
178	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
179	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
180	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
181	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
182	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
183	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
184	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
185	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
186	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
187	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
188	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
189	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
190	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
191	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
192	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
193	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
194	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
195	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
196	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
197	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
198	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
199	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	
200	23	5	5	23.1	Q23118	Primer PAVC-BLBC for	1.7	

[illegible]

400	5.3	73.3	1.67319	Anti-HCC antibody
401	5.3	73.3	74.732	Anti-CD19 antibody
402	5.3	73.3	74.732	Anti-CD19 antibody
403	5.3	73.3	74.732	Anti-CD19 antibody
404	5.3	73.3	74.732	Anti-CD19 antibody
405	5.3	73.3	74.732	Anti-CD19 antibody
406	5.3	73.3	74.732	Anti-CD19 antibody
407	5.3	73.3	74.732	Anti-CD19 antibody
408	5.3	73.3	74.732	Anti-CD19 antibody
409	5.3	73.3	74.732	Anti-CD19 antibody
410	5.3	73.3	74.732	Anti-CD19 antibody
411	5.3	73.3	74.732	Anti-CD19 antibody
412	5.3	73.3	74.732	Anti-CD19 antibody
413	5.3	73.3	74.732	Anti-CD19 antibody
414	5.3	73.3	74.732	Anti-CD19 antibody
415	5.3	73.3	74.732	Anti-CD19 antibody
416	5.3	73.3	74.732	Anti-CD19 antibody
417	5.3	73.3	74.732	Anti-CD19 antibody
418	5.3	73.3	74.732	Anti-CD19 antibody
419	5.3	73.3	74.732	Anti-CD19 antibody
420	5.3	73.3	74.732	Anti-CD19 antibody
421	5.3	73.3	74.732	Anti-CD19 antibody
422	5.3	73.3	74.732	Anti-CD19 antibody
423	5.3	73.3	74.732	Anti-CD19 antibody
424	5.3	73.3	74.732	Anti-CD19 antibody
425	5.3	73.3	74.732	Anti-CD19 antibody
426	5.3	73.3	74.732	Anti-CD19 antibody
427	5.3	73.3	74.732	Anti-CD19 antibody
428	5.3	73.3	74.732	Anti-CD19 antibody
429	5.3	73.3	74.732	Anti-CD19 antibody
430	5.3	73.3	74.732	Anti-CD19 antibody
431	5.3	73.3	74.732	Anti-CD19 antibody
432	5.3	73.3	74.732	Anti-CD19 antibody
433	5.3	73.3	74.732	Anti-CD19 antibody
434	5.3	73.3	74.732	Anti-CD19 antibody
435	5.3	73.3	74.732	Anti-CD19 antibody
436	5.3	73.3	74.732	Anti-CD19 antibody
437	5.3	73.3	74.732	Anti-CD19 antibody
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439	5.3	73.3	74.732	Anti-CD19 antibody
440	5.3	73.3	74.732	Anti-CD19 antibody
441	5.3	73.3	74.732	Anti-CD19 antibody
442	5.3	73.3	74.732	Anti-CD19 antibody
443	5.3	73.3	74.732	Anti-CD19 antibody
444	5.3	73.3	74.732	Anti-CD19 antibody
445	5.3	73.3	74.732	Anti-CD19 antibody
446	5.3	73.3	74.732	Anti-CD19 antibody
447	5.3	73.3	74.732	Anti-CD19 antibody
448	5.3	73.3	74.732	Anti-CD19 antibody
449	5.3	73.3	74.732	Anti-CD19 antibody
450	5.3	73.3	74.732	Anti-CD19 antibody

[illegible]

451	2.1	4.8	30.11	G56E48	A33 kappa light chain	5.11
452	2.1	4.8	30.11	G70E00	MAB J39D10 light chain	5.11
453	2.1	4.8	30.17	G06E69	L243 VL region 3' p21	5.11
454	2.1	4.8	30.17	G06E69	Murine IgVH light chain	5.11
455	2.1	4.8	30.17	G06E39	Anti-CD38 single chain	5.11
456	2.1	4.8	33.9	G59E13	PCR reverse primer for	5.11
457	2.1	4.8	33.9	G59E30	MAB 4197X VL gene PCR	5.11
458	2.1	4.8	35.5	G03140	IL-6R antibody primer	5.11
459	2.1	4.8	35.5	G03140	IL-6R antibody primer	5.11
460	2.1	4.8	40.12	G51112	Anti-CD45 PCR primer	5.11
461	2.1	4.8	43.12	G718993	IL-6 CD45 VL PCR primer	5.11
462	2.1	4.8	336.5	G30E81	5A8 VL	5.11
463	2.1	4.8	340.5	G30E80	phdms72.1 insert.	5.11
464	2.1	4.8	340.5	G30E80	Anti-CD38 single chain	5.11
465	2.1	4.8	726.18	G70E023	Anti-CD38 single chain	5.11
466	2.1	4.8	726.18	G70E023	Anti-CD38 single chain	5.11
467	2.1	4.8	776.10	G70E24	Anti-CD38 single chain	5.11
468	2.1	4.8	776.10	G70E24	Anti-CD38 single chain	5.11
469	2.0	4.6	70.10	G310726	Anti-CD38 single chain	5.11
470	2.0	4.6	20.32	G75E58	Primer MNC for kappa	2.7
471	2.0	4.6	20.5	G317773	M/CX primer to amplify	2.7
472	2.0	4.6	20.5	G317773	Primer-6 to probe for	2.7
473	2.0	4.6	20.6	G56E19	PCR primer for kappa	2.7
474	2.0	4.6	20.9	G56E23	PCR primer for kappa	2.7
475	2.0	4.6	20.9	G56E23	PCR primer for kappa	2.7
476	2.0	4.6	21.33	G75E10	Primer M/Calpha.	2.7
477	2.0	4.6	21.33	G75E10	Kappa light chain var	2.7
478	2.0	4.6	21.33	G75E10	Human/murine light chain	2.7
479	2.0	4.6	21.34	G75E174	Chromosomal monkey Ig	2.7
480	2.0	4.6	21.35	G75E165	Chromosomal monkey Ig	2.7
481	2.0	4.6	30.25	G10E02	Sequence of 5' primer	2.7
482	2.0	4.6	30.25	G10E02	Sequence of 5' primer	2.7
483	2.0	4.6	32.34	G72E040	Primer MYC 4' for anti	2.7
484	2.0	4.6	32.46	G70E16	Interleukin-6 helix D	2.7
485	2.0	4.6	32.46	G70E16	Interleukin-6 helix D	2.7
486	2.0	4.6	32.46	G70E16	Interleukin-6 helix D	2.7
487	2.0	4.6	32.37	G05E333	PCR primer CIG 24 for	2.7
488	2.0	4.6	32.37	G05E333	light chain primer 4	2.7
489	2.0	4.6	32.37	G76E929	Primer RYV-10R for T	2.7
490	2.0	4.6	32.37	G76E929	PCR primer for kappa	2.7
491	2.0	4.6	32.37	G76E929	PCR primer for kappa	2.7
492	2.0	4.6	35.38	G06E48	Monoclonal antibody 6	2.7
493	2.0	4.6	35.38	G75E981	Monoclonal antibody 6	2.7
494	2.0	4.6	35.38	G75E981	Monoclonal antibody 6	2.7
495	2.0	4.6	35.38	G75E981	Monoclonal antibody 6	2.7
496	2.0	4.6	35.17	G03174	Anti-IL-8 MAb 66d.2.5 va	2.7
497	2.0	4.6	35.17	G03174	Anti-IL-8 MAb 66d.2.5 va	2.7
498	2.0	4.6	57.17	G06E189	Human antibody kappa	2.7
499	2.0	4.6	57.17	G06E189	Human antibody kappa	2.7
500	2.0	4.6	194.5	G30E07	Complementarity deter	2.7
501	2.0	4.6	315.40	G19E55	Antibody L2D2-11-VL ch	2.7

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502	20	4.6	315.40	V183767	Antibody IgM/2-6-31-V	2.70e-04
503	20	4.6	328.38	T863040	Coding sequence for h	2.70e-04
504	20	4.6	339.10	Q44811	MBP NBS1 light chain	2.70e-04
505	20	4.6	339.10	Q44811	Light chain variable	2.70e-04
506	20	4.6	340.6	3137776	Light chain variable	2.70e-04
507	20	4.6	378.39	V01094	Humanized light chain	2.70e-04
508	20	4.6	403.2	Q24791	Anti-Tac antibody 119	2.70e-04
509	20	4.6	403.2	Q05601	Anti-Tac light chain	2.70e-04
510	20	4.6	413.39	T76622	Light chain transcrip	2.70e-04
511	20	4.6	413.39	T76622	Light chain variable	2.70e-04
512	20	4.6	413.39	T76622	Light chain variable	2.70e-04
513	19	4.4	18.24	T30551	Mouse kappa J region	1.35e-04
514	19	4.4	30.11	Q67714	Primer for amplifica	1.35e-04
515	19	4.4	30.11	Q67714	Primer for amplifica	1.35e-04
516	19	4.4	39.45	Q94672	Human antibody OHS-9	1.35e-04
517	19	4.4	41.21	T18988	Human anti-human IL-	1.35e-04
518	19	4.4	43.13	Q75868	Primer NRV4 for amp	1.35e-04
519	19	4.4	43.13	Q75868	Primer NRV4 for amp	1.35e-04
520	19	4.4	44.10	Q58582	Kappa light chain pr	1.35e-04
521	19	4.4	44.10	Q58582	Mouse light chain pr	1.35e-04
522	19	4.4	44.10	Q58582	Mouse light chain pr	1.35e-04
523	19	4.4	44.10	Q58582	Chappa primer to cons	1.35e-04
524	19	4.4	44.10	Q58582	Chappa primer to cons	1.35e-04
525	19	4.4	47.11	Q66760	Primer for amplifica	1.35e-04
526	19	4.4	47.11	Q66760	Primer for amplifica	1.35e-04
527	19	4.4	50.9	Q57535	PCR primers C1C 76 for	1.35e-04
528	19	4.4	50.9	Q57535	PCR primers C1C 76 for	1.35e-04
529	19	4.4	51.16	Q94540	Linker anti-epitope	1.35e-04
530	19	4.4	72.17	Q98844	Anti-human IL-4 human	1.35e-04
531	19	4.4	80.16	Q48335	MBP 25D1 light chain	1.35e-04
532	19	4.4	80.16	Q48335	Single chain Fv fram	1.35e-04
533	19	4.4	85.15	Q94962	Humanized antibody V	1.35e-04
534	19	4.4	85.15	Q94962	Human immunoglobulin	1.35e-04
535	19	4.4	153.34	T73439	Human immunoglobulin	1.35e-04
536	19	4.4	156.34	T73439	Human immunoglobulin	1.35e-04
537	19	4.4	310.4	Q28259	PopII light chain 19C	1.35e-04
538	19	4.4	315.38	T88885	Alpha light chain nuc	1.35e-04
539	19	4.4	321.7	Q42268	Encoded kappa chain V	1.35e-04
540	19	4.4	321.7	Q42268	Human antibody 3H11	1.35e-04
541	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04
542	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04
543	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04
544	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04
545	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04
546	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04
547	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04
548	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04
549	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04
550	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04
551	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04
552	19	4.4	321.7	Q51814	Antibody light chain	1.35e-04

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706	18	4.1	506.5	Q11361	PCR- β 2-M μ 13	6.60e-01
705	18	4.1	527.1	M31448	Rehepated IL16 chain D	6.60e-01
704	18	4.1	530.3	T21236	Humanized IL16 chain D	6.60e-01
703	18	4.1	608.1	M80500	Light chain antibody	6.60e-01
702	18	4.1	611.1	M16163	Sequence of humanized	6.60e-01
701	18	4.1	612.10	Q56560	Genomic sequence of c	6.60e-01
700	18	4.1	603.10	Q33793	Sequence encoding the	6.60e-01
703	18	4.1	707.39	V17379	Humanized antibody 80	6.60e-01
704	18	4.1	705.39	V17315	Humanized heavy chain	6.60e-01
705	18	4.1	709.39	V17315	Humanized heavy chain	6.60e-01
706	18	4.1	716.39	V17315	Humanized heavy chain	6.60e-01
707	18	4.1	746.24	T43437	Rehepated CD4 antibody	6.60e-01
708	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
709	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
710	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
711	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
712	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
713	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
714	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
715	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
716	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
717	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
718	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
719	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
720	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
721	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
722	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
723	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
724	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
725	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
726	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
727	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
728	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
729	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
730	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
731	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
732	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
733	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
734	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
735	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
736	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
737	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
738	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
739	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
740	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
741	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
742	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
743	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
744	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
745	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
746	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
747	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
748	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
749	18	4.1	748.24	Q33568	Rehepated CD4 antibody	6.60e-01
750	18	4.1	748.24	Q33568	Rehepated CD4 antibody	

807	16	3.7	40.36	Q49456	oligomer m45 used to	3.05e+00
806	16	3.7			Anti-human influenza	3.05e+00
805	16	3.7			Antibody 4D2.17 v4	3.05e+00
804	16	3.7			B3 immunoglobulin var	3.05e+00
803	17	3.9	336.24	717997	Humanised mouse anti-	3.05e+00
802	17	3.9	381.32	759502	Humanised 5C7.29 anti-	3.05e+00
801	17	3.9	384.21	715537	Humanised 12A1 anti-	3.05e+00
800	16	3.7	35.13	715537	Anti-CD45 VL coding	3.05e+00
799	16	3.7	386.11	Q69181	Humanised Hsp27 light	3.05e+00
798	17	3.9	386.11	Q65523	Anti-V4A SYD9 V-kap	3.05e+00
797	17	3.9	386.12	Q67346	Humanised anti-V4A	3.05e+00
796	17	3.9	386.37	V02235	Humanised anti-V4A	3.05e+00
795	17	3.9	386.37	V02235	Anti-V4A-4 humanised	3.05e+00
794	17	3.9	386.11	Q65527	Humanised Hsp27 light	3.05e+00
793	17	3.9	386.11	Q65527	Anti-human IL-4 human	3.05e+00
792	17	3.9	406.34	717486	Alpha 4 integrin huma	3.05e+00
791	17	3.9	406.34	717486	Sequence encoding var	3.05e+00
790	17	3.9	406.34	717486	Chimeric MAb 15 P6m	3.05e+00
789	17	3.9	406.34	717486	Levay v antibody 326	3.05e+00
788	17	3.9	699.11	716700	Humanised 5Gc1.1 v+	3.05e+00
787	17	3.9	711.21	708486	Single-chain anti-erb	3.05e+00
786	17	3.9	711.28	705006	Sequence encoding tcd	3.05e+00
785	17	3.9	711.18	Q57128	Humanised 5Gc1.1 v+	3.05e+00
784	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
783	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
782	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
781	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
780	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
779	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
778	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
777	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
776	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
775	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
774	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
773	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
772	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
771	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
770	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
769	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
768	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
767	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
766	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
765	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
764	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
763	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
762	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
761	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
760	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
759	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
758	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
757	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
756	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
755	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.05e+00
754	17	3.9	726.11	710706	Humanised 5Gc1.1 v+	3.0

C	808	16	3, 7	40 17	C939303	Humanized anti-VLA-4	1,3se01
C	809	16	3, 7	41 3	C939303	Kappa variable region	1,3se01
C	810	16	3, 7	43 8	T575370	PCR primer CIG-28 for	1,3se01
C	811	16	3, 7	43 8	T575370	PCR primer CIG-28 for	1,3se01
C	812	16	3, 7	44 27	C939504	Humanized anti-VLA-4	1,3se01
C	813	16	3, 7	42 24	T780100	Primer (B3-L2) for am	1,3se01
C	814	16	3, 7	42 6	C939599	PCR primer B3-L2 for am	1,3se01
C	815	16	3, 7	42 11	T046555	Mouse derived RT-PCR	1,3se01
C	816	16	3, 7	42 11	T046555	Sequence of one of th	1,3se01
C	817	16	3, 7	42 9	C958203	Primer oligo 25 for h	1,3se01
C	818	16	3, 7	50 38	T868505	Anti-human IL-4 Mab h	1,3se01
C	819	16	3, 7	50 11	C939951	Anti-human IL-4 Mab h	1,3se01
C	820	16	3, 7	52 37	T868336	Primer for variable h	1,3se01
C	821	16	3, 7	52 37	T868336	Primer for variable h	1,3se01
C	822	16	3, 7	52 18	T159122	Humanized IL2 Mab VF	1,3se01
C	823	16	3, 7	54 18	T161938	Humanized antibody H1	1,3se01
C	824	16	3, 7	72 3	C104668	SCA gene linker mb12	1,3se01
C	825	16	3, 7	72 3	C103893	Primer 312-65	1,3se01
C	826	16	3, 7	76 11	C634522	RTI human Ab L chain	1,3se01
C	827	16	3, 7	77 13	C440077	RTI human Ab L chain	1,3se01
C	828	16	3, 7	77 13	C440077	RTI human Ab L chain	1,3se01
C	829	16	3, 7	79 9	C755450	Humanized antibody V/	1,3se01
C	830	16	3, 7	79 13	C755450	Humanized antibody V/	1,3se01
C	831	16	3, 7	84 8	C483440	Anti-human IL-4 human	1,3se01
C	832	16	3, 7	106 17	C939495	Anti-human IL-4 human	1,3se01
C	833	16	3, 7	100 24	T437356	Primer 3090 for human	1,3se01
C	834	16	3, 7	121 21	T165644	Human M64 antibody 11	1,3se01
C	835	16	3, 7	135 24	T734335	Human laminoogluclan	1,3se01
C	836	16	3, 7	135 24	T734335	Human laminoogluclan	1,3se01
C	837	16	3, 7	253 1	C066230	VR domain of antibody	1,3se01
C	838	16	3, 7	253 2	C066230	VR domain of antibody	1,3se01
C	839	16	3, 7	253 29	T635508	Monoclonal antibody D	1,3se01
C	840	16	3, 7	253 29	T635508	Monoclonal antibody D	1,3se01
C	841	16	3, 7	259 36	T437244	Anti-DNA antibody 821	1,3se01
C	842	16	3, 7	259 36	T437244	Anti-DNA antibody 821	1,3se01
C	843	16	3, 7	259 30	T437343	Anti-DNA antibody 523	1,3se01
C	844	16	3, 7	297 30	T437399	Anti-DNA antibody 15b	1,3se01
C	845	16	3, 7	297 30	T437399	Anti-DNA antibody 15b	1,3se01
C	846	16	3, 7	320 30	T437432	Anti-DNA antibody 15b	1,3se01
C	847	16	3, 7	318 23	T280313	Humanized antibody va	1,3se01
C	848	16	3, 7	318 23	T280313	Humanized antibody va	1,3se01
C	849	16	3, 7	318 38	T868835	Alpha light chain nuc	1,3se01
C	850	16	3, 7	321 39	T868835	Alpha light chain nuc	1,3se01
C	851	16	3, 7	321 39	V137000	Humanized antibody 80	1,3se01
C	852	16	3, 7	321 34	V173101	Humanized antibody 80	1,3se01
C	853	16	3, 7	321 34	V173101	Humanized antibody 80	1,3se01
C	854	16	3, 7	321 30	T438062	Anti-DNA antibody 821	1,3se01
C	855	16	3, 7	321 30	T438062	Anti-DNA antibody 821	1,3se01
C	856	16	3, 7	321 30	T773370	Anti-Receptor-IX human1	1,3se01
C	857	16	3, 7	322 6	C483230	MAB 25D2 Vb CDNA	1,3se01
C	858	16	3, 7	322 6	C483230	MAB 25D2 Vb CDNA	1,3se01
C	859	16	3, 7	322 6	C483230	MAB 25D2 Vb CDNA	1,3se01
C	860	16	3, 7	322 6	C483230	MAB 25D2 Vb CDNA	1,3se01

859	16	3.7	324.34	CDNA encoding light c	1.34e+01
860	16	3.7	324.31	Anti-TOF beta-1 scFv	1.34e+01
861	16	3.7	324.35	Anti-TOF beta-2 scFv	1.34e+01
862	16	3.7	324.4	Human IgG2 receptor-b1	1.34e+01
863	16	3.7	324.45	Human IgG2 receptor-b2	1.34e+01
864	16	3.7	325.12	Light chain of Ab-01	1.34e+01
865	16	3.7	323.11	Light chain variable	1.34e+01
866	16	3.7	323.12	Human IgG2 receptor-b1	1.34e+01
867	16	3.7	323.13	Murine 206 antibody	1.34e+01
868	16	3.7	329.40	Interleukin-5 humans	1.34e+01
869	16	3.7	339.18	Humanized L23 Mab VK	1.34e+01
870	16	3.7	339.37	Variable kappa chain	1.34e+01
871	16	3.7	339.46	L23 Mab VK region DNA	1.34e+01
872	16	3.7	339.48	Humanized L23 Mab VK	1.34e+01
873	16	3.7	339.29	R21 humanized 206 ant	1.34e+01
874	16	3.7	340.12	Murine L chain from M	1.34e+01
875	16	3.7	341.28	Coding sequence for I	1.34e+01
876	16	3.7	341.3	Humanized L chain	1.34e+01
877	16	3.7	342.3	Hyposensitized antigen	1.34e+01
878	16	3.7	342.3	Murine kappa chain va	1.34e+01
879	16	3.7	342.11	Mouse HNRG1 light cha	1.34e+01
880	16	3.7	345.1	Humanized L chain	1.34e+01
881	16	3.7	345.1	Variable L chain	1.34e+01
882	16	3.7	351.13	Anti-interleukin-4 mo	1.34e+01
883	16	3.7	372.32	Immunoglobulin F101-7	1.34e+01
884	16	3.7	381.32	Human anti-human Fas	1.34e+01
885	16	3.7	381.32	Human anti-human Fas	1.34e+01
886	16	3.7	386.13	Human anti-human Fas	1.34e+01
887	16	3.7	387.7	FK2 (VMD) VJ coding	1.34e+01
888	16	3.7	390.9	Humanized Mab 2502.11	1.34e+01
889	16	3.7	393.3	Humanized Mab 2502.11	1.34e+01
890	16	3.7	393.3	Mab 2502 humanized	1.34e+01
891	16	3.7	399.13	CDR-grafted L243-9L1	1.34e+01
892	16	3.7	399.11	Sequence encoding the	1.34e+01
893	16	3.7	402.18	Humanized anti-His tag	1.34e+01
894	16	3.7	402.18	Emulsification antigen	1.34e+01
895	16	3.7	402.2	Humanized anti-His tag	1.34e+01
896	16	3.7	407.4	Humanized anti-His tag	1.34e+01
897	16	3.7	409.11	Humanized anti-His tag	1.34e+01
898	16	3.7	409.11	Humanized anti-His tag	1.34e+01
899	16	3.7	439.33	CDNA encoding humans	1.34e+01
900	16	3.7	439.33	CDNA encoding humans	1.34e+01
901	16	3.7	504.12	CDNA encoding wild ty	1.34e+01
902	16	3.7	504.12	CDNA encoding wild ty	1.34e+01
903	16	3.7	642.40	Humanized anti-His tag	1.34e+01
904	16	3.7	642.26	Humanized anti-His tag	1.34e+01
905	16	3.7	646.72	Humanized anti-His tag	1.34e+01
906	16	3.7	646.72	Humanized anti-His tag	1.34e+01
907	16	3.7	699.11	Humanized anti-His tag	1.34e+01
908	16	3.7	702.13	Humanized anti-His tag	1.34e+01
909	16	3.7	705.39	Humanized heavy chain	1.34e+01

910	16	3, 7	729	12	Q73679	Fv(CP-4) immunosuppre	1,34e-01
911	16	3, 7	727	13	Q73678	Fv(CP-2) immunosuppre	1,34e-01
912	16	3, 7	737	13	T94606	EcoRI-HindIII insert	1,34e-01
913	16	3, 7	731	10	T66433	pBR 4.12 insert encod	1,34e-01
914	16	3, 7	737	10	T66433	intracellular binding	1,34e-01
915	16	3, 7	810	20	T27010	Glycophorin antibody	1,34e-01
916	16	3, 7	870	10	Q67396	SCP sequence in vec	1,34e-01
917	16	3, 7	889	3	Q21098	SCP sequence in vec	1,34e-01
918	16	3, 7	889	3	Q21098	SCP anti-lysozyme	1,34e-01
919	16	3, 7	895	13	Q76272	SCP anti-lysozyme	1,34e-01
920	16	3, 7	900	39	V12612	Human DNA fragment vx	1,34e-01
921	16	3, 7	900	28	T31182	DNA fragment V65, 6	1,34e-01
922	16	3, 7	900	12	Q44234	Human DNA fragment vx	1,34e-01
923	16	3, 7	900	12	Q44234	Human DNA fragment vx	1,34e-01
924	16	3, 7	915	1	Q04466	Light chain variable	1,34e-01
925	16	3, 7	923	15	Q91988	Pv restriction fragme	1,34e-01
926	16	3, 7	923	12	T59129	Single chain, humanis	1,34e-01
927	16	3, 7	960	3	Q21601	Gene encoding Omp of	1,34e-01
928	16	3, 7	960	3	Q21601	Salmonella secreted p	1,34e-01
929	16	3, 7	1023	30	T67030	Salmonella secreted p	1,34e-01
930	16	3, 7	1175	37	T68311	Single chain anti-dia	1,34e-01
931	16	3, 7	1175	37	T68311	Single chain anti-dia	1,34e-01
932	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
933	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
934	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
935	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
936	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
937	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
938	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
939	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
940	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
941	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
942	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
943	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
944	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
945	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
946	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
947	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
948	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
949	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
950	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
951	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
952	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
953	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
954	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
955	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
956	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
957	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
958	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
959	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
960	16	3, 7	1175	12	Q70663	SCP-BSRNAS fusion D	1,34e-01
961	16	3,					

[illegible]

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PD 35-APR-1989.
PF 16-APR-1989: 303814.32
PF 17-APR-1989: 303814.32
PA (Title) BILLY AND CO
PI Beaver LS, Bunoil TP, Gadeki RA, Weigel RJ;
DR WP1: 89-11120/43.
PR P-PSB08: p59035. cgdg, producing antibodies - monoclonal and
P7 Chimeric derived from monoclonal antibody K53/4.
P8 Claim 1: page 43, 8pp; English.
P9 The DNA encodes the light chain of monoclonal antibody K53/4, used to
CC which binds human chimeric antibodies. K53/4 is a murine antibody
CC which binds human C regions around immunological problems during treatment.
SC Sequence 639 BP: 175 C: 149 G: 141 T:
Query Match 19 33; Gapd 84; PB 1; Length 639;
Best Local Similarity 100.0%; Score 96.5; E-Val: 6D;
Mismatches 0; Indels 0; Gaps 0
M80 Conservative 0 Mismatches 0
Db 260 cognatcgcgtctggagggggacacttgcaataaacaggcgatgcgaaccact 339
Oy 343 CGCGACAGCTGCTGGAGGGGACACTTGCATAATTAACCGGTCACTGCCAACCAC 402
Db 340 gattccatctctcccacccaacctgac 363
Oy 403 CATCCACATCTCCCAACAACCAACAACT 426
RESULTS
AC 085387 standard: cDNA, 465 BP.
DT 31-AUG-1993 (first entry)
DE MAD 43379.1 light chain variable region.
KM AIGHA-SYCNFGLKTHAL; 198nt chain; variable region; antibody;
KN AIGHA-SYCNFGLKTHAL; 198nt chain; variable region; epithelial cell.
KS PM819; 43379. monoclonal antibody; Ab; ds
OS Synthetic.
CS Key Location/Qualifiers
FT CDS 1
FT ID=1 /tag=a
PR MO503828-A.
PR 09-FEB-1995. U07919
PR 02-AUG-1993: US 101329.
PA (R0USV) HOUSTON BIOTECHNOLOGY INC.,
DI Sould, BM, Kellinher Pj, Wallace TL, Wood HS;
DI D1 Sould, BM, Kellinher Pj, Wallace TL, Wood HS;
DR P-PSB08: R70282.

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P7	extracellular catalact extraction.
P8	Dilution:
P9	Disaccharide; p16 p1; 68bp; English;
CC	Catalactin (given in R0527) completes the heavy (VH) and light
CC	chain (VL) regions of the alpha-2-microglobulin gene cluster
CC	linked to ricin A-chain encoding the VL and VH regions of 419X
CC	(O05519/-88, respectively) were obtained from hybridoma mRNA,
CC	amplified by PCR, and engineered for inclusion in the immunotoxin
QY	sequence (465 bp). 118 A; 115 C; 115 G; 116 T.
Query Match	
E	Similarity 100%; Score 83; DB 14; Length 465;
Hatches	83 Conservative 0 Missmatch 0 Indels 0 Gaps 0
Bb	361 cgttcgcgagggggcgcccaaccgcctgaagaacaggcgcgcacccatgcccca 440
Oy	350 ccccaccc 409
	441 ttttccccccccctccgaagaacct 463
Oy	410 ttcttcaccaacaattcacagtgnccgrr 432
RESULT	
ID	10
AD	standard: cDNA to mRNA; 882 BP.
AO	048038
DE	08-FEB-1993 (first entry)
DT	Monoclonal antibody M(Alpha)-L-3 L-chain coding sequence.
DD	antigenase small neurotoxic protein antibody; kappa; light chain;
KW	cyclohexal agitat; aa;
FH	Key Location/Ovalifiers
FT	signal_peptide 1..36
FT	cde 1..678 a
FT	/tag b
FT	/product -lg_light-chain
FT	mab_peptide 3...354
FT	/product -lg_variable_region
FT	mab_peptide 35...675
FT	/tag d
FT	/product -lg_constant_region
PF	EP-556111.A.
PD	18-AUG-1993.
PP	09-FEB-1993. 400323.
PA	IHEU/COLAATM-001505.
PA	(COMS) COMISSARIAT ENERGIE ATOMIQUE.
P1	Roulet J, Ducaenel F, Gallier D, Menes A;
RP	WP1: j91.360519/33.

[illegible]


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P1 S6L1-precursor chlamid polypeptide comprising biologically active
P2 sequence and single-chain antibody sequence - has resistance to e.g.
P3 degrading temperature, presence of proteolytic enzymes, etc.
P4
P5 The present invention is the CDNA which encodes immunoglobulin (Ig) light
P6 chain variable region of a murine anti-asparaginase II monoclonal
P7 antibody (mAb). The cDNA was used in the preparation of a novel
P8 recombinant chimeric polypeptide, comprising a rat region
P9 containing a biological epitope, linked via a polypeptide to a
PCC region including an antibody variable region (SCV) having the light and heavy
PCC regions of an antibody variable region which specifically binds the antigen
PCC region and protects its biological activity from denaturation by
PCC conformation in which the SCV is bound to a polypeptide assumes a
PCC denaturing temperatures or pH conditions. proteolytic enzymes,
PCC polypeptides inherent to form a trispartite complex consisting of
PCC antibody-light chain complex. A Trispartite-S6L1 fusion protein of
PCC the above type has better thermal resistance than free
S0 Sequence 360 BP; 85 A; 102 C; 87 G; 86 T;
Query Match
S1 Start: 16.1%; Score 70; DB 37; Length 360;
Matches 30; Conserved: 0; Mismatches 0; Indels 0; Gaps 0
Db 231 CAGCTTCGGGAGGCGGCACGAAGTGTGAATAAAGCAAGCGTGATGGCAGCATCTATC 350
Oy 348 CAGCTTCGGGAGGCGGCACGAAGTGTGAATAAAGCAAGCGTGATGGCAGCATCTATC 407
Db 351 catctcccaca 360
Oy 408 CATCTCCCA 417
RESULT:
16
DB 769346 standard: CDNA; 1848 BP.
DT 08-Apr-1998 (first entry)
DI Chlamic gene containing anti-asparaginase NAB light and heavy chain.
IM Immunoglobulin Ig; heavy chain; variable region; murine; human;
FM recombinant chimeric polypeptide; NAB; light chain;
OS synthetic; chimeric polipeptide; ss.
OC Chlamic - Homo sapiens.
PN DB586570-A.
PF 21-Nov-1997.
PR 22-Dec-1993; 447432.
OR

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21. JMN-1988; US-105748.
PR
21. KOL-1982; US-335955.
PR
21. HIRSH-1976; US-385927.
PA (HRR)- HYBRIDOMA LTD.
P1 Ramessingh M, Rothenstein A, Shani ET;
DM WEP-958700/51.
The present invention relates to chimeric polypeptide comprising biologically active P1 sequence and murine anti-aspartyl aminopeptidase resistance to e.g. P7 disrupting temperature, presence of proteolytic enzymes etc.
Example 2: Columns 27-30; 28pp: English.
CC The present sequence is a chimeric gene containing the cDNA for the CC asparaginase II. The gene was used in the preparation of a novel CC recombinant chimeric polypeptide, comprising a lat region CC containing an epitically active domain and another domain CC including a single chain antibody (SCA) having the light and heavy chain of an antibody variable region which specifically binds the antigen. In the lat region the chimeric polypeptide assumes a conformation, in the lat region the biological activity of the lat region and protects its biological activity against degradation by denaturing agents or alcohol. The regions of the chimeric CC containing aspartyl aminopeptidase and pH conditions, proteolytic enzymes, CC antibody-antigen complex formation, Lysine structure analogous to an CC sequence 184d BP; 435 N; 498 C; 517 G; 398 T;
DQ

Query Match 16.1% Score 70: DN 37, Length 146d,
Beat Local Statistic 100.0% Pref No. 2,83e+66,
Matrix 70: Conservative 0; Missatches 0; Indels 0; Gaps 0

Dh 23c acatgcagggagggacgacgaggaattatgaaacgtccctgatcttcgcaaacatgcatc
Gy 348 CAGCTGGCGGCGGCGGCACATCGTGAAATTAATTCACGCCGTCAATCTCCACCATCTGATC 407
Db 351 catcttcccaca 360
Dh |||||
Gy 408 CATCTTCCA 417

RESULT 17
ID T94625 standard; DNM: 270 bp.
DC 234625-1996 (first entry)
DE Mouse derived latent chain R23 phase antibody pattern A DNA
FN Latent chain: R23; murine: catalytic antibody; bacteriophage;
NM pattern A; ss.

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DP      055334284-A.
DP      05-0201-1993.
DP      06-FEB-1993; US-831967.
PP      06-FEB-1993; US-831967.
PP      07-OCT-1993; US-131804.
PA      (CHIR) CHIRON CORP.
PI      Houston, TX; CHIRON-COLINAS INC.
PI      Houston, TX; Harsco US.
DR      P-DESD: 96-03319/4/33.
DR      P-DESD: W02280.
CC      complete, coding, antisense, targeting antibody fragment constructs -
CC      PT constructs.
CC      Example 1: Columns 31-35, 30pp1, 30pp2, 30pp3, 30pp4, 30pp5, 30pp6, 30pp7, 30pp8, 30pp9, 30pp10, 30pp11, 30pp12, 30pp13, 30pp14, 30pp15, 30pp16, 30pp17, 30pp18, 30pp19, 30pp20, 30pp21, 30pp22, 30pp23, 30pp24, 30pp25, 30pp26, 30pp27, 30pp28, 30pp29, 30pp30, 30pp31, 30pp32, 30pp33, 30pp34, 30pp35, 30pp36, 30pp37, 30pp38, 30pp39, 30pp40, 30pp41, 30pp42, 30pp43, 30pp44, 30pp45, 30pp46, 30pp47, 30pp48, 30pp49, 30pp50, 30pp51, 30pp52, 30pp53, 30pp54, 30pp55, 30pp56, 30pp57, 30pp58, 30pp59, 30pp60, 30pp61, 30pp62, 30pp63, 30pp64, 30pp65, 30pp66, 30pp67, 30pp68, 30pp69, 30pp70, 30pp71, 30pp72, 30pp73, 30pp74, 30pp75, 30pp76, 30pp77, 30pp78, 30pp79, 30pp80, 30pp81, 30pp82, 30pp83, 30pp84, 30pp85, 30pp86, 30pp87, 30pp88, 30pp89, 30pp90, 30pp91, 30pp92, 30pp93, 30pp94, 30pp95, 30pp96, 30pp97, 30pp98, 30pp99, 30pp100, 30pp101, 30pp102, 30pp103, 30pp104, 30pp105, 30pp106, 30pp107, 30pp108, 30pp109, 30pp110, 30pp111, 30pp112, 30pp113, 30pp114, 30pp115, 30pp116, 30pp117, 30pp118, 30pp119, 30pp120, 30pp121, 30pp122, 30pp123, 30pp124, 30pp125, 30pp126, 30pp127, 30pp128, 30pp129, 30pp130, 30pp131, 30pp132, 30pp133, 30pp134, 30pp135, 30pp136, 30pp137, 30pp138, 30pp139, 30pp140, 30pp141, 30pp142, 30pp143, 30pp144, 30pp145, 30pp146, 30pp147, 30pp148, 30pp149, 30pp150, 30pp151, 30pp152, 30pp153, 30pp154, 30pp155, 30pp156, 30pp157, 30pp158, 30pp159, 30pp160, 30pp161, 30pp162, 30pp163, 30pp164, 30pp165, 30pp166, 30pp167, 30pp168, 30pp169, 30pp170, 30pp171, 30pp172, 30pp173, 30pp174, 30pp175, 30pp176, 30pp177, 30pp178, 30pp179, 30pp180, 30pp181, 30pp182, 30pp183, 30pp184, 30pp185, 30pp186, 30pp187, 30pp188, 30pp189, 30pp190, 30pp191, 30pp192, 30pp193, 30pp194, 30pp195, 30pp196, 30pp197, 30pp198, 30pp199, 30pp200, 30pp201, 30pp202, 30pp203, 30pp204, 30pp205, 30pp206, 30pp207, 30pp208, 30pp209, 30pp210, 30pp211, 30pp212, 30pp213, 30pp214, 30pp215, 30pp216, 30pp217, 30pp218, 30pp219, 30pp220, 30pp221, 30pp222, 30pp223, 30pp224, 30pp225, 30pp226, 30pp227, 30pp228, 30pp229, 30pp230, 30pp231, 30pp232, 30pp233, 30pp234, 30pp235, 30pp236, 30pp237, 30pp238, 30pp239, 30pp240, 30pp241, 30pp242, 30pp243, 30pp244, 30pp245, 30pp246, 30pp247, 30pp248, 30pp249, 30pp250, 30pp251, 30pp252, 30pp253, 30pp254, 30pp255, 30pp256, 30pp257, 30pp258, 30pp259, 30pp260, 30pp261, 30pp262, 30pp263, 30pp264, 30pp265, 30pp266, 30pp267, 30pp268, 30pp269, 30pp270, 30pp271, 30pp272, 30pp273, 30pp274, 30pp275, 30pp276, 30pp277, 30pp278, 30pp279, 30pp280, 30pp281, 30pp282, 30pp283, 30pp284, 30pp285, 30pp286, 30pp287, 30pp288, 30pp289, 30pp290, 30pp291, 30pp292, 30pp293, 30pp294, 30pp295, 30pp296, 30pp297, 30pp298, 30pp299, 30pp300, 30pp301, 30pp302, 30pp303, 30pp304, 30pp305, 30pp306, 30pp307, 30pp308, 30pp309, 30pp310, 30pp311, 30pp312, 30pp313, 30pp314, 30pp315, 30pp316, 30pp317, 30pp318, 30pp319, 30pp320, 30pp321, 30pp322, 30pp323, 30pp324, 30pp325, 30pp326, 30pp327, 30pp328, 30pp329, 30pp330, 30pp331, 30pp332, 30pp333, 30pp334, 30pp335, 30pp336, 30pp337, 30pp338, 30pp339, 30pp340, 30pp341, 30pp342, 30pp343, 30pp344, 30pp345, 30pp346, 30pp347, 30pp348, 30pp349, 30pp350, 30pp351, 30pp352, 30pp353, 30pp354, 30pp355, 30pp356, 30pp357, 30pp358, 30pp359, 30pp360, 30pp361, 30pp362, 30pp363, 30pp364, 30pp365, 30pp366, 30pp367, 30pp368, 30pp369, 30pp370, 30pp371, 30pp372, 30pp373, 30pp374, 30pp375, 30pp376, 30pp377, 30pp378, 30pp379, 30pp380, 30pp381, 30pp382, 30pp383, 30pp384, 30pp385, 30pp386, 30pp387, 30pp388, 30pp389, 30pp390, 30pp391, 30pp392, 30pp393, 30pp394, 30pp395, 30pp396, 30pp397, 30pp398, 30pp399, 30pp400, 30pp401, 30pp402, 30pp403, 30pp404, 30pp405, 30pp406, 30pp407, 30pp408, 30pp409, 30pp410, 30pp411, 30pp412, 30pp413, 30pp414, 30pp415, 30pp416, 30pp417, 30pp418, 30pp419, 30pp420, 30pp421, 30pp422, 30pp423, 30pp424, 30pp425, 30pp426, 30pp427, 30pp428, 30pp429, 30pp430, 30pp431, 30pp432, 30pp433, 30pp434, 30pp435, 30pp436, 30pp437, 30pp438, 30pp439, 30pp440, 30pp441, 30pp442, 30pp443, 30pp444, 30pp445, 30pp446, 30pp447, 30pp448, 30pp449, 30pp450, 30pp451, 30pp452, 30pp453, 30pp454, 30pp455, 30pp456, 30pp457, 30pp458, 30pp459, 30pp460, 30pp461, 30pp462, 30pp463, 30pp464, 30pp465, 30pp466, 30pp467, 30pp468, 30pp469, 30pp470, 30pp471, 30pp472, 30pp473, 30pp474, 30pp475, 30pp476, 30pp477, 30pp478, 30pp479, 30pp480, 30pp481, 30pp482, 30pp483, 30pp484, 30pp485, 30pp486, 30pp487, 30pp488, 30pp489, 30pp490, 30pp491, 30pp492, 30pp493, 30pp494, 30pp495, 30pp496, 30pp497, 30pp498, 30pp4
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[illegible]

AC	Q54631.1	24-JUN-1994	(first entry)	
AD	784.12	1198c-chain		
AE	784.12	1198c-chain		
AF	784.12	1198c-chain		
AG	784.12	1198c-chain		
AH	784.12	1198c-chain		
AI	784.12	1198c-chain		
AJ	784.12	1198c-chain		
AK	784.12	1198c-chain		
AL	784.12	1198c-chain		
AM	784.12	1198c-chain		
AN	784.12	1198c-chain		
AO	784.12	1198c-chain		
AP	784.12	1198c-chain		
AQ	784.12	1198c-chain		
AR	784.12	1198c-chain		
AS	784.12	1198c-chain		
AT	784.12	1198c-chain		
AV	784.12	1198c-chain		
AW	784.12	1198c-chain		
AX	784.12	1198c-chain		
AY	784.12	1198c-chain		
AZ	784.12	1198c-chain		
BA	784.12	1198c-chain		
BB	784.12	1198c-chain		
BC	784.12	1198c-chain		
BD	784.12	1198c-chain		
BE	784.12	1198c-chain		
BF	784.12	1198c-chain		
BG	784.12	1198c-chain		
BH	784.12	1198c-chain		
BI	784.12	1198c-chain		
BJ	784.12	1198c-chain		
BK	784.12	1198c-chain		
BL	784.12	1198c-chain		
BM	784.12	1198c-chain		
BN	784.12	1198c-chain		
BO	784.12	1198c-chain		
BP	784.12	1198c-chain		
BQ	784.12	1198c-chain		
BR	784.12	1198c-chain		
BS	784.12	1198c-chain		
BT	784.12	1198c-chain		
BU	784.12	1198c-chain		
BV	784.12	1198c-chain		
BW	784.12	1198c-chain		
BX	784.12	1198c-chain		
BY	784.12	1198c-chain		
BZ	784.12	1198c-chain		
CA	784.12	1198c-chain		
CB	784.12	1198c-chain		
CC	784.12	1198c-chain		
CD	784.12	1198c-chain		
CE	784.12	1198c-chain		
CF	784.12	1198c-chain		
CG	784.12	1198c-chain		
CH	784.12	1198c-chain		
CI	784.12	1198c-chain		
CJ	784.12	1198c-chain		
CK	784.12	1198c-chain		
CL	784.12	1198c-chain		
CM	784.12	1198c-chain		
CN	784.12	1198c-chain		
CO	784.12	1198c-chain		
CP	784.12	1198c-chain		
CQ	784.12	1198c-chain		
CR	784.12	1198c-chain		
CS	784.12	1198c-chain		
CT	784.12	1198c-chain		
CU	784.12	1198c-chain		
CV	784.12	1198c-chain		
CW	784.12	1198c-chain		
CX	784.12	1198c-chain		
CY	784.12	1198c-chain		
CA	784.12	1198c-chain		
CB	784.12	1198c-chain		
CC	784.12	1198c-chain		
CD	784.12	1198c-chain		
CE	784.12	1198c-chain		
CF	784.12	1198c-chain		
CG	784.12	1198c-chain		
CH	784.12	1198c-chain		
CI	784.12	1198c-chain		
CJ	784.12	1198c-chain		
CK	784.12	1198c-chain		
CL	784.12	1198c-chain		
CM	784.12	1198c-chain		
CN	784.12	1198c-chain		
CO	784.12	1198c-chain		
CP	784.12	1198c-chain		
CQ	784.12	1198c-chain		
CR	784.12	1198c-chain		
CS	784.12	1198c-chain		
CT	784.12	1198c-chain		
CU	784.12	1198c-chain		
CV	784.12	1198c-chain		
CW	784.12	1198c-chain		
CX	784.12	1198c-chain		
CY	784.12	1198c-chain		
CA	784.12	11		

PN	J0101899-A.
PD	18-APR-1995.
PR	06-COR-1993:
PA	(HQC/T) NAGMANA Y WPI: 95-187987/24.
DR	P-9508: R/4/95/5.
PT	anti-human antibody against an human anticancer monoclonal pharmacology; medicine and biochemical fields.
CC	Example 5 : Page 18: 28pp: Japanese. P04945-09043 are DNA clones encoding anti-idiotypic antibodies CC monoclinal antibody. These antibodies and DNA encoding them are useful in pharmacological, medical and biochemical field of research.
SQ	Sequence 334 BP: 69 A: 95 C: 90 G: 80 T:
Query Match	12.4% Score 54; DB 16; Length 354;
Best Local Similarity	100.0%; Pvald. No. 3,12e-31;
Matches	54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dn	301 tttcccttggttgggaggaacgcgcgatataataggcattggcgtagcaaa 354 Gy 346 TACACTGCAGCACCAGCGCACCTGGATTAATAAACGCCGTATGCTCAACA 399
RESULT	30
ID	T70811 standard DNM: 429 BP.
AC	T70811
DC	3'0JUL-1997 (first entry)ii
RV	Anti-idiotypic anti-BCRB epitome light chain variable region Antid-idiotypic anti-BCRB epitoma growth factor receptor; tumour; cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacture; sa.
OS	Rna untransluc.
CDS	Location/Qualifiers 1..429 .. FT FT cdw .. FT FT /tag= a ii FT FT /note= "no stop codon given"
FT	signal_peptide 1..60 ..
FT	a..b i..j ..
FT	/tag= c i..j ..
FT	primer_bind 405..429 ..
FT	/tag= d ..
FT	EP_745612-XL ..
PD	14-MAY-1996: EP-107651
PR	26-MAR-1995: PF-107667
PA	GOMK
PI	Aidan J. Carroll&A. Gomes A. Pulats J. Rosell B.
DI	WI: 97-01659/02.

DR	P-950B;M19560.
PE	Homoelonal anti-idiotypic antibodies mimicking epidermal growth
PT	factor receptor - useful for tumour therapy
CC	Mutl. monoclonal Abp. Idiotypic antibodies, 158R, 186 and 5A5 are
CC	new. They induce an immune response against epidermal growth factor
CC	receptor (EGFR). The sequences of the heavy and light chain variable
CC	regions of these antibodies are given in the specification. The
CC	tumour that express EGFR on their surface, including melanoma,
CC	gliomas and carcinomas.
SC	sequence 429 BP: 109 A: 104 C: 100 G: 116 T:
DB	Query Match 12 4% Score 54; DB 30; Length 429;
	Beet Local Similarity 100.0%; Pval. No. 3.12e-31;
	Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	371 TGGAAATGAGCGCTCAATGCACATCATGTCATCATTCCGCCACTCCA 424
RESULT 31	ID 370807 standard; DNA: 441 BP.
AC	30-COD-1897 (clant entry)
KD	Anti-idiotypic anti-EGFR epidermal growth factor receptor; tumour;
KD	cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacture; ss.
OS	Mus musculus.
FN	cd8 location/Owalltizer
FT	/tag= 1; 441
FT	/tag= a
FT	signal_peptide 1..72 no stop codon given.
FT	primer_bind 1..31 b
FT	/tag= c
FT	primer_bind 418..441
FT	/tag= d
PI	EP-15612-A1.
PD	04-DEC-1996.
PF	14-MAY-1996: 107651.
PR	28-MAY-1995: EP-107667
PI	Adan J, Carceller A, Gomes A, Pulats O, Rissell E:
PI	WPI: 97-018659-02.
DR	P-950B; M19576.
DR	Recombinant anti-idiotypic antibodies blocking epidermal growth
DR	factor receptor used in immunotherapy
DR	Class 6; Fig 5B; 28pp; English.

[illegible]

DR WPI: 96777732/-78.
 DR Humanised monoclonal antibodies with donor framework residues 29
 and 78 . esp. against CD18, useful for treating cancer and auto-immune
 diseases.
 PS Disclosure: Figure 2: 92p; English.
 CC A monoclonal antibody (mAb) which has donor CDR's of foreign origin
 and a recipient framework (Fmk) consisting of human or primate origin where the
 Fmk is of human or primate origin.
 CC The framework is selected at position 29 or 78 of the heavy (H) chain of
 the framework as described above.
 CC That in the corresponding position of the H chain of the AB
 wherein the CDR's are derived, can be used for the treatment of cancer,
 rheumatoid arthritis, specifically multiple myeloma, lymphoma and
 carcinoma.
 CC Residue 29 and 78 of the humantized AB with the replacing framework
 residue restores the antigen binding activity of the antibodies.
 CC Sequence 364 Pst: 99 A1: 88 C1: 95 T1:
 50

Query Match 12.0%; Score 53; DB 24; Length 364;
 Best Local Similarity 98.8%; Pfad: N.2.1e-29;
 Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 282 scggaaagatgctcgaaggagggaacagactgttgaaataagaagctgccttcgaaccac 341
 097 tcccttcaagctctctcgaagggcgacacacacgtctgaaaatttttaaacggcctcatctccacacac 342
 342 tgcacatcacagtctcgaagggcgacacacacgtctgaaaatttttaaacggcctcatctccacacac 343
 407 tgcacatcacagtctcgaagggcgacacacacgtctgaaaatttttaaacggcctcatctccacacac 424

	DR	HPI:	967778/78.
	PB	Wnt1 generated monoclonal antibodies with donor framework residues 29 and	
	PT	diseases against CD38, useful for treating cancer and auto-immune	
	PS	Disease; Figure 2: 92pp English.	
	CC	A monoclonal antibody (Ab) which has donor CDR's of foreign origin	
	CC	original amino acid sequence of human or primate orIGIN where the	
	CC	framework is replaced by an amino acid the same as the chain of	
	CC	what in the corresponding position of the H chain of the Ab from	
	CC	and autumun disease-derived can be used for the treatment of cancer,	
	CC	rheumatoid arthritis. The Ab binds to CD38 protein, lymphoma and	
	CC	residues 29 and 78 of the humanised Ab with the original donor	
	SQ	Sequence 35d Pab: 39 A; 88 G; 92 G; 93 T;	
	Query Match Similarity 12.0%; Score 52; DB 24; Length 36d;		
	Monoclonal Antibody 98.8% Pfed. No. 2.1E+29;		
	Mechanism 81; Commercially 0; Mismatches 1; Indels 0; Capses 0;		
DB	282	tccggaacagctgttcggaggcgatgcagaactcagaagtgcgatgcagcatcac 341	
DB	342	tcccgaacagctgttcggaggcgatgcagaactcagaagtgcgatgcagcatcac 401	
OY	403	tgcagaccattcccccaaacccaacca 36d	
		GCATGCGCTCAACAGTCGTCCAATTGCCA CATGCA 424	
RESULT_14			
RN	standard; cDNA: 2001 BP.		
NC	Q46088		
CD	07-FEB-1994 (first entry)		
DD	sequence encoding 741 aa pV-pK0.		
NB	Single Chain PV polypeptide; "VF-VL heterodimer; immunoglobulin; Ig;		
OS	pseudomas.		
KR	Key	Location/Qualifiers	
CDS	/cds	I..2001	
F	"vFab-a"	a	
DP	MO93I185-A		
PD	19-AUG-1993		
PF	05-FEB-1993		
PP	05-FEB-1993; DO-813167		
PR	GESTAR-1993; GENPEP-COMP*		
RA	(CERN); CREATIVE BIOMOLECULES INC.		
RI	Houston TX,Hudson JS., Oppermann H, Ring DB;		
RT	WT: 93-271889; MW: 120 kDa		
TX	New single chain PV polipeptide binding to C-alpha-D-2 tumour		

[illegible]

P7	antigen - for imaging or treating breast or ovarian cancer etc.
P8	Example, page 71-74; Dfpp; English, expressed on the surface of
C6	cancer cells, such as breast and ovarian
C6	tumour cells, such as breast and ovarian
C6	approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
C6	pt. of about 3.5 (see Gd40B3, R93565). A single chain IgG antibody
C6	a gene fusion including VH and CH2 domains which is expressed from
C6	a peptide-encoding linker. Such linker sequences are set forth in
C6	1A, residues 16-115 in R93569, which includes part of the 1C 1A
C6	antibody, a single chain IgG antibody, for the 52009 monoclonal
C6	binding affinity for a c-erbB-2 related antigen in binding a
C6	peptide sequence corresponding to amino acid residues 627-642, the
C6	resulting 741g protein, a portion of the anti-c-erbB-2 IgG, p940,
C6	protein, which was constructed with an 18 residue linker per leader
SQ	sequence. 2001 Bp.; 357 A.; 649 C.; 512 G.; 343 T;
Query Match:	11.7% Score 51. DB-BP; Length 2003.
Best Local Similarity 100.0%;	Freq. No. 1; Pos:-28;
M71	51: Conservative; 0: Mismatches; 0: Indels; 0: Gaps;
D8	721s ttaaaagggcctgcgtcgccgaacatgcaacttcctcccaccatgccg 712
G7	376 yttttaaaccgcctcatcctgcacacacgtacacacgtacacacgtccacgt 426
RESULT 35	
I1	V01224 standard; DNA; 391 Bp.
ID	15-MAR-1998 (first entry)
D2	Amt IL-8-related molecule 664.2.5 light chain variable region DNA sequence
D2	Light chain; heavy chain; monoclonal antibody; interleukin 8-IL-8-
RW	Inflammatory disorder; bacterial pneumonia; neutrophil chemotaxis;
RW	Streptococcus pneumoniae; Streptococcus pneumoniae; Streptococcus pneumoniae;
RW	ulcerative colitis; ds.
MS	Bsp.
O8	
misc_feature	Location/Qualifiers
F7	1..31
F7	/tag = "encodes the variable light region"
F7	misc_feature 342..391
F7	/note = "encodes a partial constant light region"
F7	misc_difference 391
F7	/tag = "The last two amino acids of this codon are not given in the original sequence."

!!SEQUENCE_LIST 1.0
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check: 7546 from:

FROM: of: /home/obryen/ree455/olig/us08836455.seq
sequence 1, application us/08836455

general information:

applicant: chatterjee, malaya
applicant: foon, kenneth a.
applicant: chatterjee, sunil k. . .

TO: GenBank: * Sequences: 602,539 Total-length: 1,199,477,030 April 18, 1999 18:59

Database Release Information:

GenBank, Release 110.0, Released on 14Dec1998, Formatted on 15Dec1998
EMBL, Release 56.0, Released on 15Sep1998, Formatted on 15Dec1998

Word-size: 15 Words: 182747 Diagonals: 6,088 Total diagonals: 2,000,000,000
Integral-width: 1 Alphabet: 4 List-size: 50 CPU minutes: 116.94

Sequence Stnd Diag Score Width Documentation ..

GB_RO:MMISKCC	+	5	332	1	141880 Mus musculus immunoglobulin ka
GB_PAT:AR007981	+	339	306	1	AR007981 Sequence 5 from patent US 57
GB_PAT:123446	+	339	306	1	123446 Sequence 5 from patent US 5534
GB_RO:AF045508	+	0	305	1	AF045508 Mus musculus dc10 anti-poly
GB_RO:MMUSX	+	-60	304	1	L48667 Mus musculus (cell line C3H/F2
GB_RO:AF045510	+	0	298	1	AF045510 Mus musculus 6C9 monoclonal
GB_RO:AF045495	+	0	294	1	AF045495 Mus musculus dc4 anti-poly
GB_RO:MMU55591	+	-68	291	1	U55591 Mus musculus anti-DNA immunog
GB_RO:MMISGAC1	+	252	284	1	U00565 Mouse Ig kappa active gene: Vx
GB_RO:MMIGK7	+	253	284	1	V00808 Part of the murine gene for ka
GB_RO:MMU55588	+	-69	281	1	U55588 Mus musculus anti-DNA immunog
GB_RO:MMISG1AFA	+	-78	280	1	M36246 Mouse Ig kappa-chain mRNA V re
GB_RO:AF003293	+	225	273	1	AF003293 Mus musculus Ig kappa light
GB_RO:MMISGKVC	+	253	273	1	V00566 Mouse Ig kappa germline V gene
GB_RO:MMIGK3	+	253	273	1	V00804 Murine kappa-immunoglobulin ge
GB_PAT:107835	+	-75	273	1	M64168 Mus musculus Ig active kappa-c
GB_PAT:107835	+	-60	271	1	U07835 Sequence 4 from patent EP 0088
GB_PAT:103643	+	-60	271	1	U03643 Sequence 4 from patent US 4642
GB_PAT:103643	+	-60	270	1	U29617 Mus musculus anti-DNA antibody
GB_RO:MMU29617	+	-63	268	1	M59920 Mouse Ig germline chain mRNA V
GB_RO:MMISGKAA3	+	42	266	1	U88675 Mus musculus anti-DNA antibody
GB_RO:MMU88675	+	-60	265	1	X63811 M.musculus mRNA for IgM V(K)M
GB_RO:MMVKKRB11	+	-19	249	1	X02177 M.musculus mRNA for IgG kappa
GB_RO:MMIGGVJ1	+	-60	245	1	U30236 Mus musculus anti-DNA antibody
GB_RO:MMU30236	+	-75	241	1	U88676 Mus musculus anti-DNA antibody
GB_RO:MMU88676	+	-60	241	1	Z22118 M.domesticus Igk variable regi
GB_RO:MMIGKVB5	+	-10	233	1	M12191 Mouse Ig active kappa-chain VJ
GB_RO:MMISGKCA	+	-60	232	1	X82890 M.musculus Iggl, light chain V
GB_RO:MMIGG1VL	+	-60	230	1	U25098 Mus musculus anti-Pseudomonas
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GB_RO:SS69053	+	218	229	1	AF003294 Mus musculus Ig kappa light
GB_RO:AF003294	+	-18	226	1	X02178 M.musculus mRNA for IgG kappa
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GB_RO:MMU62776	+	-84	210	1	U19320 Mus musculus immunoglobulin ka
GB_RO:MMU19320	+	-60	206	1	AF003291 Mus musculus IgG kappa light
GB_RO:AF003291	+	-60	203	1	AF003299 Mus musculus IgG kappa light
GB_RO:AF003299	+	-97	197	2	U21066 Mus musculus immunoglobulin ka
GB_RO:MMU21066	+	-60	196	1	AF023475 Mus musculus anti-pneumolys
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GB_RO:MMOSIGKVE	+	486	190	2	U00568 mouse Ig kappa unproductively
GB_RO:MMOSIGKAE	+	486	190	2	V00760 Mouse pseudogene for kappa-lm
GB_RO:MMIGG04	+	10	182	1	AB016620 Mus musculus mRNA for Immun
GB_RO:AB016620	+	-78	182	1	X03382 Mouse mRNA for GAT (HP27) anti
GB_RO:MMIGKCA1	+	-60	180	1	X90902 M.musculus antibody light cha
GB_RO:MMALCVR27	+	-60	178	1	AF003300 Mus musculus IgG kappa light
GB_RO:AF003300	+	-57	178	1	SS5170 nitrophenyl phosphate-specif
GB_RO:SS5170	+	-114	175	1	U19327 Mus musculus immunoglobulin ka
GB_RO:MMU19327	+	-84	174	1	X03383 Mouse mRNA for GAT (HP22) anti
GB_RO:MMIGKGA2	+	-105	162	1	X03384 Mouse mRNA for GAT (HP29) anti
GB_RO:MMIGKGA3	+	-126	156	1	U19326 Mus musculus immunoglobulin ka
GB_RO:MMU19326	+				

of sequences containing matches at least 15 nucleotides long

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[illegible]

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409	39	9	0	336	MDGIC309	M. musculus IgE	1.33e-11
410	39	9	0	336	MDGIC309	M. musculus IgE	1.33e-11
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420	39	9	0	179	MDGIC309P	M. musculus IgE	1.33e-11
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                                     /organism="Mus musculus"
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Query Match          28.0%   Score 122; DB 29; Length 684;
Best Local Similarity 98.9%;   Pval. 6.01e-112;
Matches 181; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Oy      163 ATCTGTGCGACGAGCCAGTCGCATCAATCATTTAAAGCAGTCAATCCGCGACGACGACGATTA 222
Db      475 GATTCTGTGCGACGAGCCAGTCGCATCAATCATTTAAAGCAGTCAATCCGCGACGACGACGATTA 534
Oy      223 GGTTCTGTGCGACGAGCCAGTCGCATCAATCATTTAAAGCAGTCAATCCGCGACGACGACGATTA 282
Db      535 ATTGCGACTGCTGAATGCTGATCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 594
Oy      283 ATTGCGACTGCTGAATGCTGATCAATTTAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 342
Db      595 CGCT 598
Oy      343 CCGT 346

RESULT      9
LOCUS       HMKIK7               685 bp      DNA           ROD
DEFINITION Part of the murine gene for kappa-immunoglobulin leader sequence.
ACCESSION   U02134
VERSION     92133
KEYWORDS    differentially expressed gene; Ig kappa light chain; immunoglobulin.
SOURCE      mouse.
ORGANISM    Mus musculus
Eukaryote; Euteleostomi; Eumetazoa; Chordata; Rodentia; Scuriophaga; Myomorphi; Muridae;
Muriinae; Mus.
REFERENCE   1 (bases 1 to 685)
AUTHORS    A. Kapra, J. Immunoglobulin and leader, P.
TITLE      Recombination without further somatic mutation
JOURNAL    Nature 280 (5721), 370-375 (1979).
COMMENTARY EST DDB|U02134|MOSK1.
FEATURES
            Location/Qualifiers
             .. 1.. 685

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[illegible]

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	Query/Match
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	Matches 150; Conservation: 0; Mismatches 1; Indels 0; Gaps 0;
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Oy	163 TGGCTGCGAGCAGACCAATGAATTCAGTAAAGCCGTATACGCACATCCCATTTA 222
Db	223 GATTTCGTCTCCCCAAAAGCTTAGTGAGAGCGTGTGCGAGATTAATTCCTCAC 288
Oy	223 GATTTCGTCTCCCCAAAAGCTTAGTGAGAGCGTGTGCGAGATTAATTCCTCAC 282
Db	283 ATACACAGCCTTACAGTCAACAATTTTTCG 313
Oy	283 ATACACAGCCTTACAGTCAACAATTTTTCG 313
RESULT 14	
LOCUS	HMG5591 328 bp mRNA ROD
DEFINITION	HMG5 mouse RFL-1 DNA Immunoglobulin light chain Igc, antibody
ACCESSION	G55591 partial cdf.
NID	91870287
SOURCE	mouse
ORGANISM	house mouse
	Mus musculus
	Eukaryotes; Mitochondrial eukaryotes; Metazoa; Chordata;
	Vertebrates; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
REFERENCE	1 (bases 1 to 328)
AUTHORS	Kirihara,M.,N., Jou,H.-T., and Marion,T.N.
TITLE	Correlation for DNA among semantically derived VH-CD3 structures and
JOURNAL	specificity for DNA among autoimmune antibodies to DNA
REFERENCE	2 (bases 1 to 328)
AUTHORS	Marion,T.N.
TITLE	Direct sequencing
JOURNAL	Microbiol./Immunology 1986) Toy N. Marion, Dept. of
	Microbiology/immunology, university of Tennessee, 858 Madison Ave,
	Memphis, TN 38103, USA
FEATURES	Location/Qualifiers
source	/organism='Mus musculus'
	/strain='(H2K x NEW) F1'
	/note='mouse number 363'
	/cell_line='J65.73'
	/cell_type='hybridoma'
V-region	<1...>328

[illegible][illegible][illegible][illegible]

[illegible]

	ORGANISM	Hit description
		Mus musculus
		Embryonized; Althochondriai eukaryotes; Metazoa; Chordata;
		Artiodactyla; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
		Mus musculus
REFERENCE		1 (bases 1 to 306)
AUTHORS		Wheathoff C.H., Wylie D.E., Kathol S., Whittier A., McHugh J. and
TITLE		Shuttle D.D.
JOURNAL		Unpublished
REFERENCE		2 (bases 1 to 306)
AUTHORS		Wheathoff C.H., Wylie D.E., Kathol S., Whittier A., McHugh J. and
TITLE		Shuttle D.D.
JOURNAL		Unpublished
FEATURES		Location/Qualifiers
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		organism="Mus musculus"
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		/db_xref="taxon:10090"
		/cell_line="HLA2"
		1..306" /position=""
CD3		<1..306
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		/frame_id=-1
		/db_xref="PDB:5J052419"
		/translation="CPSPSLASLCAENYSLTCAADQIGSSLWMLQCEPQVITRIYLIY
		ATSSLDQVRRFGRGSGEDSLITSSIFSESDPYVCLQVASSPFGGTTLEIR
BASE COUNT	78 a	71 c 72 g 85 t
ORIGIN		
Query Match	22.5%	Score 98; DB:39; Length 306;
Similarity 98		
Matches 128; Conservative 0;		Matches 0; Indels 0; Gaps 0;
		Matches 0; Mismatches 0;
D5	88	TGGCTTCAAGACAGACATGATATTAACCGCTATCTACGCCATCACTACGATTGTA 147
D6	148	GATTCCTGATGCTCCCAAAAGATCTGACGCGCATGACGCTCGGTGATATTTCTCTCAC 207
D7	163	TGGCTTCAAGACAGACATGATATTAACCGCTATCTACGCCATCACTACGATTGTA 222
D8	223	GATTCCTGATGCTCCCAAAAGATCTGACGCGCATGACGCTCGGTGATATTTCTCTCAC 282
D9	208	ATCCAGCAC 316
Dy	283	ATCCAGCAC 381
RESULT	19	

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          ma_peptide  91.  >456
          /product='Laminoglobulin kappa-chain'
BASE COUNT      118 A      114 C      108 G      116 T
ORIGIN
Query Match      20 93;  Score 91;  DB 29;  Length=456;
          115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130
Matches  91.  Conserved?  0;  Mismatch?  0;  Indels  0;  Gaps  0
Dh  356  TAGGTCGCGTCAACGCTGTGGACGGGCGACCAACGCTGAATATTAACCGGCTGATGCTGCTGC
Oy  336  TAGGTCGCGTCAACGCTGTGGACGGGCGACCAACGCTGAATATTAACCGGCTGATGCTGCTGC
          395  ACCACATGTAATTCATATTCACCAACCACTCACT 426
Oy  396  ACCACATGTAATTCATATTCACCAACCACTCACT 426

RESULT  21
SUBS  1000336      293 bp      mRNA      ROD      18-OCT-1995
DEFINITION  Homo sapiens adult testis V-j kappa chain mRNA, V-J region,
ACCESSION  U30236
VERSION  9895170
KEYWORDS  T cells
SOURCE  Homo sapiens
ORGANISM  Homo sapiens
Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae
REFERENCE  1 (bases 1 to 293)
AUTHORS  Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.E.
TITLE  Light chain gene targeting to specificity in anti-DNA antibodies
REFERENCE  2 (bases 1 to 293)
AUTHORS  Ibrahim,S.M., Weigert,M., Basu,C., Erikson,J. and Radic,M.E.
TITLE  Direct Substitution
JOURNAL  Submitted (3-20-1995)
FEATURES
     location: 31-300-1995)
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     /db_xref='taxon:10090'
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     41...293
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     /product='Ig kappa chain'
     /db_xref='PDB:9895171'

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BASE COUNT	72 a	71 c	66 g	82 t	2 others
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Query Match	Best Local Similarity: 99.74%; Pctd. No. 1.38e-74;				
Matches	1020: Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
Dh	103 TGGCTGAGACAGACACAGATGACATGATACACCGCTATGACAGATGATTA 162				
Gy	163 TGGCTGAGACAGACACAGATGACATGATTAACCGCTATGACACACATGATTA 232				
Dh	163 GATTCGCTGCTCCCAAAAGCTGATGCGGACAGCGCGGGTGAATATTTTCTCCAC 232				
Gy	223 GCTTCGCTGCTCCCAAAAGCTGATGCGGACAGCTGCGGGTGAATATTTCTCCAC 282				
Dh	223 A 232				
Gy	283 A 283				
RESULT 32	133991 438 bp DNA				
LOCUS	DEFINITION Sequence 45 from patent US 5589573.				
ACCSSION	U13991782				
KEYWORDS	91803782				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 438)				
AUTHORS	Haghighi, R. and Akhtar, Y.				
TITLE	Anti-cancer human monoclonal antibody and DNA base sequences				
JOURNAL	Patent: US 5589573 A 43 31-DEC-1996.				
FEATURES	Location/Qualifiers				
source	1..438				
BASE COUNT	104 a 120 c 112 g 102 t				
ORIGIN	104 a 120 c 112 g 102 t				
Query Match	20.74; Score 90; DB 29; Length 293;				
Matches	Best Local Similarity: 100%; Pctd. No. 1.38e-74;				
Matches	90: Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Dh	334 TACACCTTGAGAGGGGAGACAGCTGCGAATTAACGGCGCTGATCTGCACACACTGA 353				
Gy	346 TACACCTTGAGAGGGGAGACAGCTGCGAATTAACGGCGCTGATCTGCACACACTGA 405				

Db	334	TCCATCTTCCTCAGCATGCAATGCATGG	423
Cy	406	TCCATCTTCCTCAGCATGCAATGCATGG	435
RESULT	33		
AD	E09035	standard: RN: MOD: 438 BP.	
AL	E09035		
BI	E09035		
NI	d1107372		
DT	08-OCT-1997 (Ref. 52, Created)		
DF	08-OCT-1997 (Ref. 52, Last updated, Version 1)		
DE	antibody named Idiot1 chain variable region of mouse antidiotype		
DI	antibody named Idiot1 against CLN-19c Idiotype.		
OS	Mus musculus (house mouse)		
NC	Synonym(s): Muscaea; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia;		
OC	Eumetazoa; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia;		
PC	(1) 438		
BP	1-438		
RA	Hajimura H., Moriwaka Y.,		
RT	MONOCLONAL ANTIBODY AND DNA BASE SEQUENCE CODING FOR THE SHM μ		
RL	Patent number JP 1995101999-N/7, 18-Apr-1995.		
HL	HAGIMURA TOSHITAKE		
PR	JP 1995101999-N/7 (mouse)		
PD	18-Apr-1995		
CC	PF 08-OCT-1993 JP 1993272950		
CC	HAGIMURA HIDETAKI, AKASHI YASUTORI		
CC	CIJ2R1.91*, CIJ2R9.10, CIGNR9.02, CIJ2P1.09, CIJ2P2.08, CIJ2P3.08,		
CC	CIJ2R1.91*, CIGNR9.10, CAGNR9.02, CIJ2P1.09, CIJ2P2.08, CIJ2P3.08,		
CC	strand(s): Double:		
CC	Topology: Linear:		
CC	Hypothetical: No:		
CC	Key		
PH	sense: No:		
CH	Location/Qualifiers		
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FT	1..438		
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FT	/clone="Idiot1"		
FT	alg_peptide		
FT	1..339		
FT	40..438		
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FT	antidiotype		
FT	antibody named Idiot1 against CLN-19c		
FT	idiotype		
FT	40..438		
FT	Fragment 1 of light chain variable		
FT	region of Idiot1?		
FT	106..153		
FT	misc_feature		

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	CC	FT	/note=Fragment 2 of light chain variable
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	CC	FT	210..215
	CC	FT	/note=Fragment 3 of light chain variable
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	CC	FT	/note=CDB3 of light chain variable region of Idioty7
	CC	FT	340..369
	CC	FT	/note=Fragment 4 of light chain variable
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	CC	FT	Location/Qualifiers
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	FT	Sequence	438 bp; 104 M; 110 C; 112 G; 102 T; 0 other;
	FT	Query Match	20.7%; Score 90; DP 10; Length 438;
	FT	Best Local Similarity	100.0%; Pctd. No. 1,188-74;
Dh	Matches	90: Conservative 0; Mismatches 0; Indels 0; Caps 0;	
Dh	334	TACAGCTTCGCGAAGCAAGTGTATTTAAAGGGCTGCATCTGCACACTCTGA	393
Oy	346	TACAGCTTCGCGAGGGGAGCAAGTGCTGATTAAAAGGGCTCATCTGCACACTCTGA	405
Dh	394	TCCATCTGCCACATCAGTAAGTCTTGGG	423
Oy	406	TCCATCTGCCACATCAGTAAGCTTGGG	435
RESULT	24	AF001393	570 bp DNA ROD 24-JAN-1998
LOCUS	DEFINITION	Mus musculus Ig kappa 1 light chain variable region gene, partial cds	
ACCSSION	NID	C0131393	
KEYWORDS	RID	G310644	
SOURCE	ORGANISM	house mouse Mus musculus	
REFERENCE	AUTHORS	Bukacinski W, Krawiec M, Krawiec J, Chodryda J, Vertehesi I, Mamulaia E, Orlowski H D., Moore P L. and Schulz P.G.	
	REMARKS	1 (bases 1 to 570)	
		Redentis / Scunymouth; Muridae; Murinae; Mus.	
JOURNAL		Immunogenetics 47 (1) 91-95 (1998) 18k-v9 gene family	

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US-08-836-455-1.rge
Nov Apr 19 13:23:48 1999

REFERENCE          1 (bases 1 to 471)
AUTHORS            Peter J., Pellegrini M.J., Soughon R., Tello D., Poljak R.J.,
TITLE              Crystal structure of a cross-reaction complex between Fab P9.13.7
SYNOPSIS           3 Biol. Chem. (1995) In press
REMARKS            3 Biol. Chem. (1995) In press
AUTHORS            Peterson N.C.
TITLE              Direct Submission
JOURNAL            Submitted (03-NR-1995) Norman C. Peterson, Pathology and
                  Microbiology Research, University of Pennsylvania School of Medicine,
                  3601 Locust Walk, Philadelphia, PA 19104, USA
FEATURES
source             Location/Qualifier
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                  /feature_location="SIS1SLDNRVTSICRSADQISWYLMTCRPPGCVALLITRTS
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Query Match       19.5% Score 85; DB 29; Length 471;
Mismatch          85; Conservative   0; Mismatches 0; Indels 0; Gaps 0;
DB 258 TCCTGACACGCTGCGAAGGGGACCAAGCTGCTGAATAAAAGGGGCTATCTGCCAACAC 317
DB 342 TCCTGACACGCTGCGAAGGGGACCAAGCTGCTGAATTAACACGGGACTCATCTGCACCAAC 401
DB 318 TCCTGACACGCTGCGAAGGGGACCAAGCTGCTGAATTAACACGGGACTCATCTGCACCAAC 401
DB 402 TCCTGACACGCTGCGAAGGGGACCAAGCTGCTGAATTAACACGGGACTCATCTGCACCAAC 426
RESULT            31

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[illegible][illegible]

LOCUS	MM101A	882 bp	RNA	ROD	30-SEP-1993
DESCRIPTION	IMMAGULAE mRNA FOR MONOCLONAL ANTIBODY				
ACCESSION	9406234				
KEYWORDS	IMMUNOGLOBULIN KAPPA LIGHT CHAIN.				
ORGANISM	HOUSE MOUSE.				
REFERENCE	1 (bases 1 to 882)				
JOURNAL	HOPKINS, F.D.				
AUTHORS	2 (bases 1 to 882)				
TITLE	DIRECT SUBMISSION				
JOURNAL	DE SAEDEY, J. (1993) F.F.D. DUCANCEL, C.E.A. DISP BAT 157, CEN				
FEATURES	OF SAEDEY, J. (1993) F.F.D. DUCANCEL, C.E.A. DISP BAT 157, CEN				
source	1. .882				

[illegible]

Query Match	18 61	Score 81	DB 29	Length 882
Best Local Similarity 100.0%		Prod. No. 2,726-64		
Matches	81: Conservative	0: Missmatches	0: Indels	0: Gaps
Db	319	THACGGTCGACGGGGGACACACATCGAATTAACCGCGCTGATGCTGATACACATCTA	378	
	346	THACGCTTCGACGGGGGACACACACGCGAATTAACCGCGCTGATGCTGATACACATCTA	405	

DB	376	TCGACATCCGACCAACCAT 399			
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RESULT	43				
LOCUS		310 bp	DNA	ROD	02-SEP-1996
DEFINITION		18 kb	1901, 1586 chain variable region.		
ACCESSION		X69890			
KEYWORDS		91524145			
REMARKS		101: kappa chain; light chain; variable region.			
ORIGIN		house mouse			
ORIGINISM		mouse			
		Eukaryotes; Eukaryotes; Eukaryotes; Metazoa; Chordata;			
		Vertebrate; Mithocera; Rodentia; Sciurognathi; Muridae; Murinae;			
REFERENCE		Niu, Yuesan 1 to 330			
AUTHORS		Nevairo-Toulon I, Paradis-Houy G, Bernards T, Martin M.,			
TITLE		Plethomya W., Shire D., Paul B. and Bied-Plethomy W.			
		Expression in <i>Escherichia coli</i> of soluble and M13 phase-displayed			
		antigenic fragments of a monoclonal antibody fragment specific for diognan			
		assessing transgenic antibody fragment specific for diognan			
		Immunotechnology 1 (1): 41-52 (1995)			
JOURNAL		95800653			
REMARK		Erratum: (published erratum appears in Immunotechnology 1995			
		2 (bases 1 to 330)			
REFERENCE		2 (bases 1 to 330)			
AUTHORS		Nevairo-Toulon I.			
TITLE		Direct Submission			
JOURNAL		Genbank (1994) 1 Nevairo-Toulon, GNS ONR 9921 Faculte de			
		Pharmacie, 15 Avenue Charles Flahault, F-94060 Montpelier Cedex			
		01, FRANCE			
FEATURES		Location/Qualifiers			

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V_region      <1 .>330
COUNT        /product=*variable region of kappa light chain of IgG1*
IN            88 a 76 c 83 g 83 t

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Best Local Similarity 10.0%   Pred. No. 3.83e-65:
Matches 80:   Conservative 0:   Nlmskats 0:   Indels 0:   Caps
Db 174 00CCCAAAGGCTTCAAGTCACAGTAAAGGCTCTGGATGATATATCTCTCAATCAGCAAGCT 233
      1111111111111111111111111111111111111111111111111111111111111111
07 234 00CCCAAAGGCTTCAAGTCACAGTAAAGGCTCTGGATGATATATCTCTCAATCAGCAAGCT 293

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[illegible][illegible]

JOURNAL
 MEDLINE
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 SOURCE
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 /db.xref="taxon:10090"
 /clone="H1d-17"
 /cell_type="epidemic B cell hybridoma"
 /development="adult"
 <1. >161
 /product="immunoglobulin kappa light chain variable
 /db_xref="PID:613991"
 /translation="VQLTQASQDQSLNLMHAGPQSHRLRLTATSLDVPFPER
 SGRSGDYSGLTSLPQVDTGCTGSGPLTATGATLPS"
 66 a 36 c 64 g 75 f
 Query Match 17.2% Score 75: DB 29: Length 261:
 Blast local similarity 100.0%: Pval: No. 1.77e-157
 Matches 75: Conserved: 0: Mismatches 0: Indels 0: Gaps 0:
 Db 123 NAAAGCTGATGTCGACAGTGGCTGCGAGGATTTCTCTGACACAGAGACCTGATG 164
 QY 239 NAAAGCTGATGTCGACAGTGGCTGCGAGGATTTCTCTGACACAGAGACCTGATG 298
 Db 185 CTCGACATTTGTCG 139
 QY 299 CTCGACATTTGTCG 313
 RESULT 50
 LOCUS 559053 295 bp 17. RNA ROD 22-SEP-1994
 DEFINITION 15 v kappa -anti-p.tiropophenyl phosphonate esterolytic antibody
 ntpep chain variable region [clone CN205] (mice, mRNA partial). 295
 ACCESSION 559053
 NID 9545318
 FEATURES
 SOURCE Mus sp.
 ORGANISM Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata:

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REFERENCE      Vertebrate: Butharia; Rodentia: Eucyonagathi; Muridae: Murinae:
AUTHORS       Mus. (beas 1 to 385)
TITLE         Differences from D.P.G., Tavil's P.S., Zahay R. and Green P.S.
              Differences in the biochemical properties of esteroyletic antibodies
              correlate with structural diversity
JOURNAL        Mol. Immunol. 31 (2), 127-137 (1994)
ENTRY          Genbank asist at the National Library of Medicine created this
              entry [ncbi gisdbd 144395] from the original journal article.
              This sequence comes from Fig. 2.
FEATURES
SOURCE         Locos300/Mallikarj
gene           /organism='Mus sp.'
               /db_xref='taxon:10095'
               1..285
               /misc_feature='[anti-phosphoryl] phosphonate esterolytic antibody
               kappa chain variable region'.
               /gene='Vg Vabgr.'.
               2..295
               /gene='Vg Vcdapab>'.
               /note='This sequence comes from Fig. 2.'
               /codon_start=1
               /protein_coding=yes
               /translation='SSASLALDEWYSYLRASRGTSGLTSLMDQNGDITRELIYALA
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BASE COUNT    73 a
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               71 g
               81 t
ORIGIN
Query Match   Query Match
Blast Local Similarity 98.5% Prd No. 1.7e-57;
Database 1357 Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 158 AAAAGGCTCAGGGACGATGGGTTCGACGATTTCCATGCACCAACGACGCTTAG 217
Cy 238 AAAAAAGCTCAGGGACGATGGGTTCGACGATTTCCATGCACCAACGACGCTTAG 297
Db 218 TCTCATATTTCGACGATTAATCTCTTGCAATATCCATATCTCCGACGACGA 277
Cy 298 TCTCATATTTCGACGATTAATCTCTTGCAATATCCATATCTCCGACGACGCA 357
Db 278 GGCGAAGCAAGCTTACA 294
Cy 358 GGCGAAGCAAGCTTACA 374

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Page 81

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[illegible][illegible][illegible]

[illegible]

97 33 CCAAGTATGACATCCAACTAACCAGCATTCCA GC

RESULT 23	AAB19112	530 bp	mRNA
DOCID	D8639	EST	17-FEB-1998
DEFINITION	UI-R-30-ap-e-12-0-U1 rat brain poly(A ⁺) RNA; cDNA sequence.		
DESCRIPTION	UI-R-30-ap-e-12-0-U1 is similar to ophiactin [AF101046 Rat] 5' active kappa-chain mRNA VJC-region from Immunocytooma IR2, mRNA sequence.		
ACCESSION	AAB19112		
RAPD	G2488938		
CROSS REFS			
SOURCE	Norway rat.		
TISSUE	Fetus nonpregnant.		
ORGANISM	Eukaryotes; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathae; Muridae; Murinae; Rattus.		
REFERENCE	Bondalid,M.F., Lennon G. and Soares,M.B.		
AUTHORS	Normalisation and subcloning: two approaches to facilitate gene discovery.		
TITLE	Genomic DNA library preparation: cloning strategy.		
JOURNAL	Journal of Molecular Biology		
MEDLINE	9704447[Ab. 6 (9). 791-806 (1996)]		
COMMENT			

Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
451 Eastland Medical Research Building Iowa City, IA 52242, USA
Tel. 319 335 8230
Fax. 319 335 9585
E-mail: msoares@uiowa.edu

This sequence has been deposited in the CDNA between the NCBI site and the oligo-dT track (not shown) served to identify it as a clone from the normalised adult lung library. cDNA Library Preparation: M.
Petras Bondalid, Ph.D. Clone distribution: clones will be available
upon request.
Seq primer: MJ Forward,
Location/Qualifiers

1..530
/define=ratna nonpregnant*
/strain=Sprague-Dawley
/note=Vector: pTZ19-Pac (Pharmacia) with a modified polymerase I site.; Not 1 Site.; Eco RI; This library contains six hundred independently cloned, normalized inserts ranging in size from approximately 1 kb to 3 kb. The tag is a string of 3-5 nucleotides present between the multiple end of the library or origin of a clone within the mixture.*
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/clone=U1-R-30-ap-e-12-0-U1*

[illegible][illegible]

NRD 9186749

EST.

SOURCE

ORGANISM

REFERENCE

NOTES

1 (bases 1 to 345)

Human

Human

Human

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NRD 9186749

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NOTES

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NRD 9186749

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SOURCE

ORGANISM

REFERENCE

NOTES

1 (bases 1 to 345)

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/sex="male"
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ORIGIN
Query Match      4.43: Score 19; DB 24; Length 363;
Best Local Similarity 100.00; Pwd. No. 2.83e+07;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Caps 0;
DB 288 CTCCTCAGATCAGACGCT 306
OY 275 CTCCTCAGATCAGACGCT 293

Search completed: Sat Apr 17 16:41:45 1999
Job time : 1470 secs.

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!!SEQUENCE LIST 1.0
(Peptide) WORDSEARCH of: /home/obryen/free455/olig/us-08-836-455-2 check: 4259 from: 1

FROMIG of: /home/obryen/free455/olig/US08836455.pep
sequence 2, application us/08836455

general information:
applicant: chatterjee, malaya
applicant: toon, kenneth a.
applicant: chatterjee, sunil k. . .

TO: pir: * Sequences: 116,738 Total-length: 37,460,341 April 18, 1999 13:58

Database Release Information:

NBRF, Release 58.0, Released on 30sep1998, Formatted on 15dec1998

Word-size: 5 Words: 49743 Diagonals: 7,036 Total Diagonals: 54,270,613
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 4.54

Sequence Strid Diag Score Width Documentation ..

PIR1:KYMSM4	+	2	116	1	Ig kappa chain precursor V region (MC
PIR2:PI0260	+	-20	98	1	Ig kappa chain V region (anti-DNA, DE
PIR2:PI0259	+	-20	95	1	Ig kappa chain V region (anti-DNA, DE
PIR2:PI0261	+	-38	81	1	Ig kappa chain V region (anti-DNA, DE
PIR4:BA7271	+	-19	80	1	nitrophenyl phosphate-specific anti
PIR2:PH1062	+	-20	77	1	Ig light chain V region (clone 202.10
PIR2:PI0262	+	-20	77	1	Ig kappa chain V region (anti-DNA, 60
PIR1:KYMS3B	+	2	70	1	Ig kappa chain precursor V region (VK
PIR2:BA8840	+	-26	69	1	Ig kappa chain V region (HP27) - mous
PIR2:C28840	+	-26	66	1	Ig kappa chain V region (HP22) - mous
PIR2:ID2840	+	-35	64	1	Ig kappa chain V region (HP29) - mous
PIR2:SI7622	+	-28	61	1	Ig kappa chain precursor V region - mous
PIR2:D32513	+	2	56	1	Ig kappa chain precursor V region (BX
PIR2:JU0080	+	-14	52	1	Ig kappa chain precursor V region (an
PIR2:SO9365	+	-3	50	1	Ig kappa chain - mouse (fragment)
PIR2:BJ2986	+	2	49	1	Ig kappa chain precursor V region (IR
PIR2:PH1224	+	0	49	1	Ig kappa chain precursor V region (M-
PIR2:A29380	+	-6	49	1	Ig kappa chain precursor V region (AC
PIR2:A26405	+	0	49	1	Ig kappa chain V region (Ars-A) - mou
PIR2:SI4237	+	0	49	1	Ig kappa chain precursor (15C5) - mou
PIR2:AA3904	+	-1	47	1	Ig kappa chain precursor V region (5-
PIR2:SG6903	+	-20	47	1	Ig kappa chain (clone KL2.29 / KL2.35
PIR2:SI9970	+	-20	46	1	Ig kappa chain V region (M-T151) - mc
PIR2:BS0551	+	-20	46	1	Ig kappa chain V region (36-71) - mou
PIR2:C26405	+	-20	46	1	Ig kappa chain V region (3D10) - mous
PIR2:KMSAR	+	-20	45	1	Ig kappa chain V regions (anti-arsone
PIR2:PI0282	+	-20	45	1	Ig kappa chain V region (45-49, anti
PIR2:BA26405	+	-20	45	1	Ig kappa chain V region (1F6) - mous
PIR2:SG6900	+	-20	45	1	Ig kappa chain (clone KL2.18 / KL4B10
PIR2:BA2644	+	-20	44	1	Ig kappa chain V region (GPI) - mous
PIR2:SI3188	+	-20	44	1	Ig kappa chain V region - mouse (frag
PIR2:SS52447	+	0	44	1	Ig kappa chain V region - mouse
PIR2:SI1700	+	-20	44	1	Ig kappa chain V region (hybridoma NC
PIR2:BA5026	+	-20	44	1	Ig kappa chain V region, anti-idiotyp
PIR2:SI4809	+	2	44	1	Ig kappa chain V region A30 - human
PIR2:SA0353	+	-6	44	1	Ig kappa chain V-J-C region - human
PIR2:SA0313	+	-4	44	1	Ig kappa chain V-J region - human
PIR2:AA28044	+	-20	43	1	Ig kappa chain V region (22B5) - mous
PIR2:PH0087	+	-20	42	1	Ig kappa chain V region (anti-cyclosp
PIR2:SI1979	+	-20	42	1	Ig kappa chain - human (fragment)
PIR2:DA4677	+	-20	42	1	Ig kappa chain V-J region (24) - mous
PIR2:SI01320	+	0	41	1	Ig kappa chain precursor - mouse
PIR2:BA4677	+	-20	41	1	Ig kappa chain V-J region (44.1) - mc
PIR2:AA4677	+	-20	41	1	Ig kappa chain V-J region (48) - mous
PIR2:SG1980	+	-20	40	1	Ig kappa chain - human (fragment)
PIR2:SI1983	+	-20	40	1	Ig kappa chain - human (fragment)
PIR2:SI1124	+	-20	40	1	Ig kappa chain V region (clone NC5-83
PIR2:SI13703	+	-20	40	1	Ig kappa chain V region (hybridoma NC
PIR2:CA4677	+	-20	40	1	Ig light chain V-J region (419.1) - pi
PIR2:SA0369	+	1	40	1	Ig kappa chain - human

at least 5 aa long

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1-22 domain signal sequence status experimental label
3-22 domain signal sequence status experimental label
23-110 domain signal sequence status experimental label
38-112 domain immunoglobulin homology label 100%
45-110 domain immunoglobulin homology label 100%
SUMMARY
Query Match 20.0% Score 28; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 4,266-50;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 76 SCVPRKSSGSDYSLTSLSEDFV 104
CY 76 SCVPRKSSGSDYSLTSLSEDFV 104

RESULT 5
ENTRY 51722
TITLE 1g kappa chain V region - mouse
ORGANISM Mus musculus (common name house mouse)
DATE 09-May-1997
ACCESSION 51722
REFERENCE 51730
AUTHORS Jackson, J.; Roggenbom, H.R.; Griffiths, A.D.; Winter, G.
J. Mol. Biol. 1993; 226:455-468
TITLE Making antibody fragments using phage display libraries.
ABSTRACT
#molecule-type nucleic acid
#residues 1-91 label CJA
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS 1g kappa chain V region; immunoglobulin V region; immunoglobulin homology
SUMMARY
Query Match 19.3% Score 28; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1,496-47;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 48 SCVPRKSSGSDYSLTSLSEDFV 75
CY 76 SCVPRKSSGSDYSLTSLSEDFV 103

RESULT 6
ENTRY PH1052
TITLE 1g light chain V region (clone 202.105) - mouse (fragment)

FEATURE 24-89
SUMMARY #domain signal sequence status experimental label
Query Match 19.3% Score 28; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1,496-47;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 57 SCVPRKSSGSDYSLTSLSEDFV 84
CY 76 SCVPRKSSGSDYSLTSLSEDFV 103

RESULT 8
ENTRY 52953
TITLE 1g kappa chain V region (fragment)
ORGANISM Mus musculus (common name house mouse)
DATE 06-Jan-1995
ACCESSION 52953
REFERENCE 52953
AUTHORS Seymour, R.
J. Mol. Biol. 1995; 249:47-57
TITLE Submitted to the EMBL Data Library, February 1991
ABSTRACT
#molecule-type nucleic acid
#residues 1-197 label SET
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS 1g kappa chain V region; immunoglobulin V region; immunoglobulin homology
SUMMARY
Query Match 19.3% Score 28; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1,496-47;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 115 PTFGCGTLEIRNADAPVSIIPPS 142
CY 115 PTFGCGTLEIRNADAPVSIIPPS 142

RESULT 9
ENTRY 568212
TITLE 1g kappa chain V region (fragment)
ORGANISM Mus musculus (common name house mouse)
DATE 20-Mar-1998
ACCESSION 568212
REFERENCE 568212
AUTHORS Kamachi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.;
FEMS Lett. (1995) 375:373-376

ORGANISM Mus musculus (common name house mouse)
DATE 30-Sep-1993
ACCESSION 568212
REFERENCE 568212
AUTHORS Tatham, D.N.; Jou, N.T.; Hill, R.J.; Marlow, T.N.
J. Exp. Med. (1993) 176:761-779
TITLE Both IgM and IgG anti-DNA antibodies are the products of a clonally selective B cell stimulation in (NBS x NZB/F1
ABSTRACT
#molecule-type nucleic acid
#residues 1-98 label TIT
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS 1g kappa chain V region; immunoglobulin V region; immunoglobulin homology
SUMMARY
Query Match 19.3% Score 28; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1,496-47;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 56 SCVPRKSSGSDYSLTSLSEDFV 83
CY 76 SCVPRKSSGSDYSLTSLSEDFV 103

RESULT 7
ENTRY B47271
TITLE 1g kappa chain V region (fragment)
ORGANISM Mus musculus (common name house mouse)
DATE 21-Sep-1993
ACCESSION B47271
REFERENCE B47271
AUTHORS Leary, S.A.; Patten, P.A.; Schulte, P.G.
Proc. Natl. Acad. Sci. U.S.A. (1993) 90:1160-1165
TITLE A genetic approach to the generation of antibodies with
ABSTRACT
#molecule-type nucleic acid
#residues 1-108 label LBS
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS 1g kappa chain V region; immunoglobulin V region; immunoglobulin homology
SUMMARY
Query Match 19.3% Score 28; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1,496-47;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 101 PTFGCGTLEIRNADAPVSIIPPS 128
CY 115 PTFGCGTLEIRNADAPVSIIPPS 142

RESULT 10
ENTRY 537464
TITLE 1g kappa chain V region (fragment)
ORGANISM Mus musculus (common name house mouse)
DATE 06-Jan-1995
ACCESSION 537464
REFERENCE 537464
AUTHORS Duncanson, P.F.D.
J. Mol. Biol. 1995; 249:47-57
TITLE Submitted to the EMBL Data Library, February 1993
ABSTRACT
#molecule-type nucleic acid
#residues 1-215 label DIC
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS 1g kappa chain V region; immunoglobulin V region; immunoglobulin homology
SUMMARY
Query Match 19.3% Score 27; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 5,066-45;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 107 YTFGCGTLEIRNADAPVSIIPPS 133
CY 116 YTFGCGTLEIRNADAPVSIIPPS 142

RESULT 11
ENTRY PC4203
TITLE 1g kappa chain V region (fragment)
ORGANISM Mus musculus (common name house mouse)
DATE 31-Dec-1996
ACCESSION PC4203
REFERENCE PC4203
AUTHORS

FEATURE 24-89
SUMMARY #domain signal sequence status experimental label
Query Match 19.3% Score 28; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1,496-47;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 57 SCVPRKSSGSDYSLTSLSEDFV 84
CY 76 SCVPRKSSGSDYSLTSLSEDFV 103

RESULT 8
ENTRY 52953
TITLE 1g kappa chain V region (fragment)
ORGANISM Mus musculus (common name house mouse)
DATE 06-Jan-1995
ACCESSION 52953
REFERENCE 52953
AUTHORS Seymour, R.
J. Mol. Biol. 1995; 249:47-57
TITLE Submitted to the EMBL Data Library, February 1991
ABSTRACT
#molecule-type nucleic acid
#residues 1-197 label SET
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS 1g kappa chain V region; immunoglobulin V region; immunoglobulin homology
SUMMARY
Query Match 19.3% Score 28; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1,496-47;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 115 PTFGCGTLEIRNADAPVSIIPPS 142
CY 115 PTFGCGTLEIRNADAPVSIIPPS 142

RESULT 9
ENTRY 568212
TITLE 1g kappa chain V region (fragment)
ORGANISM Mus musculus (common name house mouse)
DATE 20-Mar-1998
ACCESSION 568212
REFERENCE 568212
AUTHORS Kamachi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.;
FEMS Lett. (1995) 375:373-376

ACCESSIONS PC4203
 REFERENCE Nakai, J. W.; Lee, D. I.; Choi, B. K.; Cho, W. K.; Lee, S. H.;
 #authors 5
 #journal Gene (1996) 173:257-259
 #title Cloning and characterization of cDNAs coding for heavy and
 #abstract human plasma apolipoprotein A-I.
 #accession PC4203
 #molecule-type mRNA
 #residues 1-219 #label RNA
 #cross-reference DB 029147; NID:9159423; PID:9159426
 #comment The protein is specific for human plasma apolipoprotein A-I of
 #feature High-density lipoprotein.
 #feature 1-112
 #domain V region status predicted #label VAR\
 #domain C region status predicted #label CRO
 #length 219 checksum 5881
 QUERY MATCH 17.9% Score 26; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1,67e-42;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 102 TRGCGTLEIRKADAPVPSIPSS 127
 QY 117 TRGCGTLEIRKADAPVPSIPSS 142

RESULT 12
 #type fragment
 #accession S3885
 #title Ig kappa chain - mouse (fragment)
 #authors Kripp, B.; Becker, M.; Schlack, M.
 #description Submitted to the EMBL Data Library, November 1993
 #abstract Combination of a defined specificity and desired isotype by
 #cloning of an anti ovalbumine recombinant mouse 1991/192
 #molecule-type mRNA
 #residues 1-219 #label KIP
 #cross-reference DB 029147; NID:9159423; PID:9159426
 #comment The protein is specific for human plasma apolipoprotein A-I of
 #feature High-density lipoprotein.
 #feature 1-112
 #domain V region status predicted #label VAR\
 #domain C region status predicted #label CRO
 #length 219 checksum 5881
 QUERY MATCH 17.9% Score 26; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1,67e-42;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 102 TRGCGTLEIRKADAPVPSIPSS 127
 QY 117 TRGCGTLEIRKADAPVPSIPSS 142

RESULT 14
 #type fragment
 #accession PR0445
 #title Ig kappa chain precursor V-1 region - human (fragment)
 #authors Kripp, B.; Becker, M.; Schlack, M.
 #description Submitted to the EMBL Data Library, November 1993
 #abstract Combination of a defined specificity and desired isotype by
 #cloning of an anti ovalbumine recombinant mouse 1991/192
 #molecule-type mRNA
 #residues 1-219 #label KIP
 #cross-reference DB 029147; NID:9159423; PID:9159426
 #comment The protein is specific for human plasma apolipoprotein A-I of
 #feature High-density lipoprotein.
 #feature 1-112
 #domain V region status predicted #label VAR\
 #domain C region status predicted #label CRO
 #length 219 checksum 5881
 QUERY MATCH 17.9% Score 26; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1,67e-42;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 102 TRGCGTLEIRKADAPVPSIPSS 127
 QY 117 TRGCGTLEIRKADAPVPSIPSS 142

RESULT 15
 #type fragment
 #accession PR0446
 #title Ig kappa chain precursor V-1 region - human (fragment)
 #authors Kripp, B.; Becker, M.; Schlack, M.
 #description Submitted to the EMBL Data Library, November 1993
 #abstract Combination of a defined specificity and desired isotype by
 #cloning of an anti ovalbumine recombinant mouse 1991/192
 #molecule-type mRNA
 #residues 1-219 #label KIP
 #cross-reference DB 029147; NID:9159423; PID:9159426
 #comment The protein is specific for human plasma apolipoprotein A-I of
 #feature High-density lipoprotein.
 #feature 1-112
 #domain V region status predicted #label VAR\
 #domain C region status predicted #label CRO
 #length 219 checksum 5881
 QUERY MATCH 17.9% Score 26; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1,67e-42;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 102 TRGCGTLEIRKADAPVPSIPSS 127
 QY 117 TRGCGTLEIRKADAPVPSIPSS 142

Best Local Similarity 100.0%; Pred. No. 1,67e-42;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 102 TRGCGTLEIRKADAPVPSIPSS 127
 QY 117 TRGCGTLEIRKADAPVPSIPSS 142

RESULT 13
 #type fragment
 #accession J10023
 #title Ig kappa chain precursor (R993) - mouse (fragment)
 #authors J. Exp. Med. (1998) 167:954-973
 #description Point mutations cause the somatic diversification of IgM and
 #abstract 1992a anti-phosphorylcholine antibodies.
 #molecule-type mRNA
 #residues 1-225 #label CHI
 #cross-reference DB 029147; NID:9159423; PID:9159426
 #comment The protein is specific for human plasma apolipoprotein A-I of
 #feature High-density lipoprotein.
 #feature 1-112
 #domain V region status predicted #label VAR\
 #domain C region status predicted #label CRO
 #length 219 checksum 5881
 QUERY MATCH 17.9% Score 26; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1,67e-42;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 102 TRGCGTLEIRKADAPVPSIPSS 127
 QY 117 TRGCGTLEIRKADAPVPSIPSS 142

RESULT 16
 #type fragment
 #accession S4372
 #title Ig kappa chain precursor V-1 region - human (fragment)
 #authors Kripp, B.; Becker, M.; Schlack, M.
 #description Submitted to the EMBL Data Library, November 1993
 #abstract Combination of a defined specificity and desired isotype by
 #cloning of an anti ovalbumine recombinant mouse 1991/192
 #molecule-type mRNA
 #residues 1-219 #label KIP
 #cross-reference DB 029147; NID:9159423; PID:9159426
 #comment The protein is specific for human plasma apolipoprotein A-I of
 #feature High-density lipoprotein.
 #feature 1-112
 #domain V region status predicted #label VAR\
 #domain C region status predicted #label CRO
 #length 219 checksum 5881
 QUERY MATCH 17.9% Score 26; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1,67e-42;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 102 TRGCGTLEIRKADAPVPSIPSS 127
 QY 117 TRGCGTLEIRKADAPVPSIPSS 142

RESULT 17
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 #accession S4373
 #title Ig kappa chain precursor V-1 region - human (fragment)
 #authors Kripp, B.; Becker, M.; Schlack, M.
 #description Submitted to the EMBL Data Library, November 1993
 #abstract Combination of a defined specificity and desired isotype by
 #cloning of an anti ovalbumine recombinant mouse 1991/192
 #molecule-type mRNA
 #residues 1-219 #label KIP
 #cross-reference DB 029147; NID:9159423; PID:9159426
 #comment The protein is specific for human plasma apolipoprotein A-I of
 #feature High-density lipoprotein.
 #feature 1-112
 #domain V region status predicted #label VAR\
 #domain C region status predicted #label CRO
 #length 219 checksum 5881
 QUERY MATCH 17.9% Score 26; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1,67e-42;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 102 TRGCGTLEIRKADAPVPSIPSS 127
 QY 117 TRGCGTLEIRKADAPVPSIPSS 142

10-Sep-1997
 ACCESSIONS S14237
 S14236
 AUTHORS Vandamme, A.M.; Bulens, F.; Bernat, H.; Welles, L.; Lijnen, F.R.; Golen, D. (1990) 192:767-775
 JOURNAL Biochem Biophys Res Commun
 TITLE Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer.
 accession-reference: MIM:1006173
 accession: S14237
 #molecule_type mRNA
 #residues 1-234 #label VAN
 #cross-reference: EMBL:X6334; NID:951623; PDB:951623
 KEYWORDS Immunoglobulin V region; immunoglobulin homology
 SUMMARY length 219; molecular-weight 26087; checksum 6000
 QUERY Match 15.24; Score 22; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1.4e-37;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 121 GITEKADAPVTSIPPS 142
 QY 121 GITEKADAPVTSIPPS 142

18
 RESULT C28840 #type fragment
 ENTRY 19 kappa chain V region (IgP2) - mouse (fragment)
 ORIGIN 29-Aug-1987 sequence_revision 29-Aug-1987 text_change
 DATE 16-Aug-1996
 C28840 J25114
 REFERENCES Ollier, P.; Rocca-Serra, J.; Somme, G.; These, J.; Pongereau, M.
 JOURNAL EMBO J. (1985) 4:3681-3688
 TITLE The idiotype network and the internal image: possible (anti-idiotypic) antibodies in the GAT system.
 accession-reference: MIM:8613612
 accession: C28840
 #molecule_type mRNA
 #residues 1-1101 #label OIL
 #cross-reference: superfamily Immunoglobulin V region; immunoglobulin homology
 CLASSIFICATION heterotrimer; immunoglobulin
 SUMMARY length 101; checksum 5983
 QUERY Match 13.84; Score 20; DB 2; Length 101;
 Best Local Similarity 90.9%; Pred. No. 1.0e-27;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

10-Sep-1997
 ACCESSIONS S14237
 S14236
 AUTHORS Vandamme, A.M.; Bulens, F.; Bernat, H.; Welles, L.; Lijnen, F.R.; Golen, D. (1990) 192:767-775
 JOURNAL Biochem Biophys Res Commun
 TITLE Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer.
 accession-reference: MIM:1006173
 accession: S14237
 #molecule_type mRNA
 #residues 1-234 #label VAN
 #cross-reference: EMBL:X6334; NID:951623; PDB:951623
 KEYWORDS Immunoglobulin V region; immunoglobulin homology
 SUMMARY length 219; molecular-weight 26087; checksum 6000
 QUERY Match 15.24; Score 22; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1.4e-37;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 121 GITEKADAPVTSIPPS 142
 QY 121 GITEKADAPVTSIPPS 142

18
 RESULT C28840 #type fragment
 ENTRY 19 kappa chain V region (IgP2) - mouse (fragment)
 ORIGIN 29-Aug-1987 sequence_revision 29-Aug-1987 text_change
 DATE 16-Aug-1996
 C28840 J25114
 REFERENCES Ollier, P.; Rocca-Serra, J.; Somme, G.; These, J.; Pongereau, M.
 JOURNAL EMBO J. (1985) 4:3681-3688
 TITLE The idiotype network and the internal image: possible (anti-idiotypic) antibodies in the GAT system.
 accession-reference: MIM:8613612
 accession: C28840
 #molecule_type mRNA
 #residues 1-1101 #label OIL
 #cross-reference: superfamily Immunoglobulin V region; immunoglobulin homology
 CLASSIFICATION heterotrimer; immunoglobulin
 SUMMARY length 101; checksum 5983
 QUERY Match 13.84; Score 20; DB 2; Length 101;
 Best Local Similarity 90.9%; Pred. No. 1.0e-27;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

10-Sep-1997
 ACCESSIONS S14237
 S14236
 AUTHORS Vandamme, A.M.; Bulens, F.; Bernat, H.; Welles, L.; Lijnen, F.R.; Golen, D. (1990) 192:767-775
 JOURNAL Biochem Biophys Res Commun
 TITLE Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer.
 accession-reference: MIM:1006173
 accession: S14237
 #molecule_type mRNA
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 #cross-reference: EMBL:X6334; NID:951623; PDB:951623
 KEYWORDS Immunoglobulin V region; immunoglobulin homology
 SUMMARY length 219; molecular-weight 26087; checksum 6000
 QUERY Match 15.24; Score 22; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1.4e-37;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 121 GITEKADAPVTSIPPS 142
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18
 RESULT C28840 #type fragment
 ENTRY 19 kappa chain V region (IgP2) - mouse (fragment)
 ORIGIN 29-Aug-1987 sequence_revision 29-Aug-1987 text_change
 DATE 16-Aug-1996
 C28840 J25114
 REFERENCES Ollier, P.; Rocca-Serra, J.; Somme, G.; These, J.; Pongereau, M.
 JOURNAL EMBO J. (1985) 4:3681-3688
 TITLE The idiotype network and the internal image: possible (anti-idiotypic) antibodies in the GAT system.
 accession-reference: MIM:8613612
 accession: C28840
 #molecule_type mRNA
 #residues 1-1101 #label OIL
 #cross-reference: superfamily Immunoglobulin V region; immunoglobulin homology
 CLASSIFICATION heterotrimer; immunoglobulin
 SUMMARY length 101; checksum 5983
 QUERY Match 13.84; Score 20; DB 2; Length 101;
 Best Local Similarity 90.9%; Pred. No. 1.0e-27;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

10-Sep-1997
 ACCESSIONS S14237
 S14236
 AUTHORS Vandamme, A.M.; Bulens, F.; Bernat, H.; Welles, L.; Lijnen, F.R.; Golen, D. (1990) 192:767-775
 JOURNAL Biochem Biophys Res Commun
 TITLE Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer.
 accession-reference: MIM:1006173
 accession: S14237
 #molecule_type mRNA
 #residues 1-234 #label VAN
 #cross-reference: EMBL:X6334; NID:951623; PDB:951623
 KEYWORDS Immunoglobulin V region; immunoglobulin homology
 SUMMARY length 219; molecular-weight 26087; checksum 6000
 QUERY Match 15.24; Score 22; DB 2; Length 219;
 Best Local Similarity 100.0%; Pred. No. 1.4e-37;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 121 GITEKADAPVTSIPPS 142
 QY 121 GITEKADAPVTSIPPS 142

18
 RESULT C28840 #type fragment
 ENTRY 19 kappa chain V region (IgP2) - mouse (fragment)
 ORIGIN 29-Aug-1987 sequence_revision 29-Aug-1987 text_change
 DATE 16-Aug-1996
 C28840 J25114
 REFERENCES Ollier, P.; Rocca-Serra, J.; Somme, G.; These, J.; Pongereau, M.
 JOURNAL EMBO J. (1985) 4:3681-3688
 TITLE The idiotype network and the internal image: possible (anti-idiotypic) antibodies in the GAT system.
 accession-reference: MIM:8613612
 accession: C28840
 #molecule_type mRNA
 #residues 1-1101 #label OIL
 #cross-reference: superfamily Immunoglobulin V region; immunoglobulin homology
 CLASSIFICATION heterotrimer; immunoglobulin
 SUMMARY length 101; checksum 5983
 QUERY Match 13.84; Score 20; DB 2; Length 101;
 Best Local Similarity 90.9%; Pred. No. 1.0e-27;
 Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db          21 RODIONOPSPSSAS16 36
Matches    18:Consecutive      0: Mismatches      0: Indels      0: Gaps      0:
Beat Local Similarity 100.0%; Pred. No. 5.85e-23;
18:Consecutive      0: Mismatches      0: Indels      0: Gaps      0:

Oy          19 RODIONOPSPSSAS16C 36
RESULT      25
ENTRY        540166      *type complete
ORGANISM     Homo sapiens      *organism
DATE         19-May-1994      *date
Accessions  540155      *accessions
REFERENCE    Eskin, J.; Jantsch, R.; Zachau, H.G.
              Eur. J. Immunol. (1993) 23:3248-3271.
              *journal
              Expressed human immunoglobulin chl genes and their
              *title
              540166 mutation.
              *abstract
              preliminary translation not shown
              *miscellaneous
              *molecular_type mRNA
              *protein_accession P04130, P04131,
              *sequence DBM32767
              *description heterotetramer immunoglobulin V region, immunoglobulin homology
              REMARKS      Length 107 *molecular_weight 11556 *ec_number 3.149
Query Match      11.7%; Score 17; DB 2; Length 107;
Beat Local Similarity 100.0%; Pred. No. 1.28e-20;
Matches    17:Consecutive      0: Mismatches      0: Indels      0: Gaps      0:
Db          10 TCRIDIONOPSPSSAS16 26
Oy          18 TCRIDIONOPSPSSAS16 34
RESULT      26
ENTRY        D32313      *type complete
ORGANISM     Mus musculus      *organism
DATE         21-May-1990      *date
Accessions  D32313
REFERENCE    Kottmann, R.; Strobel, R.; Baltes, R.S.; Johnson, M.E.;
              Neman, D.J.; Dutschak, M.A.; Dixon, P.J.; Theodoropoulos,
              *journal
              J. Clin. Invest. (1989) 82:852-860
              *title
              Immunoglobulin kappa light chain variable region gene complex

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ENTRY      PH1063      *type fragment
TITLE      19 IgH chain V region (clone 202.33) - mouse (fragment)
AUTHORS    T. L. Allman
J. Exp. Med. (1992) 176:761-779
KEYWORDS    30-sep-1993 *sequence *revision 30-sep-1993 *entry-change
13-Jun-1996
ACCESSIONS PH1063
REFERENCES T. L. Allman, D.M. : Jou, N.T. : Hill, R.J. : Marston, T.N.
J. Exp. Med. (1992) 176:761-779
ABSTRACT    Both anti-d and iyo anti-DNA antibodies are the products of
clonally selective B cell stimulation in (NBS x NEM)pi
mice.
accession PH1063
status     nucleic acid sequence not shown
analysis-type 1-97 *label: TIT
experimental_source B cell, strain [NBS x NEM]pi
CLASSIFICATION *superfamily immunoglobulin V region; immunoglobulin homology
TERMINUS     length 34; cytochrome 138
SYNOPSIS
Query Match 11.0% Score 16; DB 2; Length 94;
Next Local Similarity 100.0% Pctd. 2; 5.6e-18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 D10M0955555555555555 16
Cy 21 D10M0955555555555555 36

RESULT 29
ENTRY      PH1064      *type fragment
TITLE      Formal cross-reactivity of anti-DNA antibodies
AUTHORS    T. L. Allman, D.M. : Jou, N.T. : Hill, R.J. : Marston, T.N.
J. Exp. Med. (1992) 176:761-779
KEYWORDS    30-sep-1993 *sequence *revision 30-sep-1993 *text-change
13-Jun-1996
ACCESSIONS PH1071
REFERENCES T. L. Allman, D.M. : Jou, N.T. : Hill, R.J. : Marston, T.N.
J. Exp. Med. (1992) 176:761-779
ABSTRACT    Anti-DNA and iDc anti-DNA antibodies are the products of
clonally selective B cell stimulation in (NBS x NEM)pi
mice.
accession PH1065
status     nucleic acid sequence not shown
analysis-type 1-97 *label: TIT
experimental_source B cell, strain [NBS x NEM]pi
CLASSIFICATION *superfamily immunoglobulin V region; immunoglobulin homology
TERMINUS     length 34; cytochrome 138
SYNOPSIS
Query Match 11.0% Score 16; DB 2; Length 94;
Next Local Similarity 100.0% Pctd. 2; 5.6e-18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 D10M0955555555555555 16
Cy 21 D10M0955555555555555 36

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REMARKS      Immunoglobulin
SDRAWY      length 97 checksum 1339
Query Match 11.0% Score 16: DB 2: Length 97:
             11.0% Score 16: DB 2: Length 97:
             11.0% Score 16: DB 2: Length 97:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36

RESULT 30
ENTRY      526332
TITLE      Ig kappa chain V region - mouse (fragment)
ORGNAMSK   19-Mar-1998
DATE       19-Mar-1998
ACCESSIONS 526332
AUTHORS    Stark, S.E.; Caton, A.J.
JOURNAL    J. Exp. Med. (1991) 174:613-624
REFERENCE   Antigen receptor genes encode a single amino acid
            interchange in a protein epitope use structurally distinct
            variable regions
ACCESSION  526332
MOLECULE-  526332
TYPE       preliminary
RESIDUES   1-103
SEQUENCE   1-103
SDRAWY     11.0% Score 16: DB 2: Length 103:
            11.0% Score 16: DB 2: Length 103:
            11.0% Score 16: DB 2: Length 103:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36

RESULT 31
ENTRY      526331
TITLE      Ig kappa chain V region - mouse (fragment)
ORGNAMSK   19-Mar-1998
DATE       19-Mar-1998
ACCESSIONS 526331
AUTHORS    Stark, S.E.; Caton, A.J.
JOURNAL    J. Exp. Med. (1991) 174:613-624
REFERENCE   Antigen receptor genes encode a single amino acid
            interchange in a protein epitope use structurally distinct
            variable regions
ACCESSION  526331
MOLECULE-  526331
TYPE       preliminary
RESIDUES   1-103
SEQUENCE   1-103
SDRAWY     11.0% Score 16: DB 2: Length 104:
            11.0% Score 16: DB 2: Length 104:
            11.0% Score 16: DB 2: Length 104:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36
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REMARKS      Immunoglobulin
SDRAWY      length 97 checksum 1339
Query Match 11.0% Score 16: DB 2: Length 104:
             11.0% Score 16: DB 2: Length 104:
             11.0% Score 16: DB 2: Length 104:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36

RESULT 33
ENTRY      C33936
TITLE      Ig kappa chain V region (VH13) - mouse (fragment)
ORGNAMSK   08-Sep-1997
DATE       08-Sep-1997
ACCESSIONS C33936
AUTHORS    Stark, S.E.; Caton, A.J.
JOURNAL    J. Exp. Med. (1991) 174:613-624
REFERENCE   Antigen receptor genes encode a single amino acid
            interchange in a protein epitope use structurally distinct
            variable regions
ACCESSION  C33936
MOLECULE-  C33936
TYPE       preliminary
RESIDUES   1-107
SEQUENCE   1-107
SDRAWY     11.0% Score 16: DB 2: Length 107:
            11.0% Score 16: DB 2: Length 107:
            11.0% Score 16: DB 2: Length 107:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36

RESULT 34
ENTRY      PLO269
TITLE      Ig kappa chain V region (anti-DNA, 3E12YK) - mouse (fragment)
ORGNAMSK   15-Aug-1996
DATE       15-Aug-1996
ACCESSIONS PLO269
AUTHORS    Mies, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.;
            Delpeyroux, F.; Crane, R.; Hogle, J.M.
JOURNAL    Nature Struct. Biol. (1995) 2:332-340
REFERENCE   Structural analysis of the complement-binding site of a
            neutralizing antibody for type 1 poliovirus and its viral
            epitope
ACCESSION  S60066
MOLECULE-  S60066
TYPE       preliminary
RESIDUES   1-115
SEQUENCE   1-115
SDRAWY     11.0% Score 16: DB 2: Length 106:
            11.0% Score 16: DB 2: Length 106:
            11.0% Score 16: DB 2: Length 106:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36

RESULT 35
ENTRY      S60066
TITLE      Ig kappa chain V region (monoclonal antibody C3) - mouse
ORGNAMSK   23-Feb-1996
DATE       23-Feb-1996
ACCESSIONS S60066
AUTHORS    Mies, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.;
            Delpeyroux, F.; Crane, R.; Hogle, J.M.
JOURNAL    Nature Struct. Biol. (1995) 2:332-340
REFERENCE   Structural analysis of the complement-binding site of a
            neutralizing antibody for type 1 poliovirus and its viral
            epitope
ACCESSION  S60066
MOLECULE-  S60066
TYPE       preliminary
RESIDUES   1-115
SEQUENCE   1-115
SDRAWY     11.0% Score 16: DB 2: Length 107:
            11.0% Score 16: DB 2: Length 107:
            11.0% Score 16: DB 2: Length 107:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36
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ENTRY      526330
TITLE      Ig kappa chain V region - mouse
ORGNAMSK   13-Jan-1995
DATE       13-Jan-1995
ACCESSIONS 526330
AUTHORS    Stark, S.E.; Caton, A.J.
JOURNAL    J. Exp. Med. (1991) 174:613-624
REFERENCE   Antigen receptor genes encode a single amino acid
            interchange in a protein epitope use structurally distinct
            variable regions
ACCESSION  526330
MOLECULE-  526330
TYPE       preliminary
RESIDUES   1-104
SEQUENCE   1-104
SDRAWY     11.0% Score 16: DB 2: Length 104:
            11.0% Score 16: DB 2: Length 104:
            11.0% Score 16: DB 2: Length 104:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36

RESULT 32
ENTRY      526329
TITLE      Ig kappa chain V region - mouse
ORGNAMSK   13-Jan-1995
DATE       13-Jan-1995
ACCESSIONS 526329
AUTHORS    Stark, S.E.; Caton, A.J.
JOURNAL    J. Exp. Med. (1991) 174:613-624
REFERENCE   Antigen receptor genes encode a single amino acid
            interchange in a protein epitope use structurally distinct
            variable regions
ACCESSION  526329
MOLECULE-  526329
TYPE       preliminary
RESIDUES   1-104
SEQUENCE   1-104
SDRAWY     11.0% Score 16: DB 2: Length 104:
            11.0% Score 16: DB 2: Length 104:
            11.0% Score 16: DB 2: Length 104:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36

RESULT 33
ENTRY      526328
TITLE      Ig kappa chain V region - mouse
ORGNAMSK   13-Jan-1995
DATE       13-Jan-1995
ACCESSIONS 526328
AUTHORS    Stark, S.E.; Caton, A.J.
JOURNAL    J. Exp. Med. (1991) 174:613-624
REFERENCE   Antigen receptor genes encode a single amino acid
            interchange in a protein epitope use structurally distinct
            variable regions
ACCESSION  526328
MOLECULE-  526328
TYPE       preliminary
RESIDUES   1-104
SEQUENCE   1-104
SDRAWY     11.0% Score 16: DB 2: Length 104:
            11.0% Score 16: DB 2: Length 104:
            11.0% Score 16: DB 2: Length 104:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36
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REMARKS      Immunoglobulin
SDRAWY      length 104 checksum 4817
Query Match 11.0% Score 16: DB 2: Length 107:
             11.0% Score 16: DB 2: Length 107:
             11.0% Score 16: DB 2: Length 107:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36

RESULT 36
ENTRY      S60066
TITLE      Ig kappa chain V region (monoclonal antibody C3) - mouse
ORGNAMSK   23-Feb-1996
DATE       23-Feb-1996
ACCESSIONS S60066
AUTHORS    Mies, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.;
            Delpeyroux, F.; Crane, R.; Hogle, J.M.
JOURNAL    Nature Struct. Biol. (1995) 2:332-340
REFERENCE   Structural analysis of the complement-binding site of a
            neutralizing antibody for type 1 poliovirus and its viral
            epitope
ACCESSION  S60066
MOLECULE-  S60066
TYPE       preliminary
RESIDUES   1-115
SEQUENCE   1-115
SDRAWY     11.0% Score 16: DB 2: Length 107:
            11.0% Score 16: DB 2: Length 107:
            11.0% Score 16: DB 2: Length 107:
Matches 16: Conserved 0: Mismatches 0: Indels 0: Gaps 0:
QY 21 D10MTSPSSLSASLG 36
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#author: W.M.; Hoegle, J.M.
#submission: submitted to the Brookhaven Protein Data Bank, January 1995
#accession: PDB accession: 1Y-AYY crystallography, 3.0 angstroms, residues
#comments: 1-221, 5'-23-115
#classification:
#superfamily: immunoglobulin V region: immunoglobulin homology
#heteroterminals: immunoglobulin
#domain: lambda chain
#chainid: lambda chain status experimental
#length 116 scoreback 7524
DB 100 PTPGGCTGCTGATGAD 115
Query Match 11.0% Score 16; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 2,6.e-10;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 115 PTPGGCTGCTGATGAD 130
#type complete
A27594
15 kappa chain precursor V-1 region (Hain-6) - human
#common-name: kappa chain precursor V-1 region (Hain-6)
#common-id: 15-Nov-1988 sequence-version 15-Nov-1988 seqct-change
16-Aug-1996
A27594
#accessions:
#authors:
#keywords:
#journal:
#title:
#access-references: WU:8014719
#scoreback: A27594
#status: not compared with conceptual translation
#status-type: DNA 6 label GSA
#releasable: this sequence was translated from an aberrantly
#note: rearranged kappa gene from lambda-producing B cells
#genetics:
#classification:
#superfamily: immunoglobulin V region: immunoglobulin homology
#heteroterminals: immunoglobulin
#domain: lambda chain sequence status predicted #label: S1C
#length 116 signal-sequence-weight 12739 scoreback 9571
#summary
Query Match 11.0% Score 16; DB 2; Length 116;

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Db          21 ROD100MSPSS15S 36
|||||
Match 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy          19 ROD100MSPSS15S 34
|||||

RESULT      37
ENTRY       B21056 #type fragment
TITLE       19 kappa chain precursor - region (RH134) - human (fragment)
ORGANISM    03-Aug-1990 sequence revision 03-Aug-1990 seq_change
DATE        20-Mar-1998
B21056
ACCESSIONS  B21056
AUTHORS      Bentley, D. L.; Rabbitts, T. H.
JOURNAL      Cell (1988) 52:181-189
TITLE        Evolution of immunoglobulin V genes: evidence indicating that
             by exon duplication human V-kappa sequences have diverged
             from non-computed lambda.
Accession   B21056
#status     preliminary
#method     1
#analysis_type 1-117 #label BBN
#accessions DB K01321: NID-B15595: PID-B18596
CLASSIFICATION superfamily immunoglobulin V region; immunoglobulin homology
SUBMITTER   Heterickman; Immunoglobulin
            Length 117 checknum 468

Query Match 11.0%; Score 16; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 2,616-18;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db          21 ROD100MSPSS15S 36
|||||

Oy          19 ROD100MSPSS15S 34
|||||

RESULT      38
ENTRY       S41809 #type complete
TITLE       19 kappa chain precursor - region A10 - human
ORGANISM    03-Aug-1990 sequence revision 03-Aug-1990 seq_change
DATE        10-Jan-1995 sequence revision 11-Jan-1995 text_change
S41809
ACCESSIONS  S41809
AUTHORS      Huber, C.; Schnabel, K. F.; Huber, E.; Klein, R.; Meland, A.;
            Thibodeau, J.; Lamm, R.; Zachau, R. G.
REFERENCE   Eur. J. Immunol. (1989) 19:2865-2875
JOURNAL
AUTHORS

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01 title
02 The V(kappa) genes of the L regions and the repertoire of V
03 (kappa) gene sequences in the human germ line.
04 accession
05 G41009
06 status
07 Preliminary
08 molecule_type DNA
09 residues 1-117
10 labels HVB
11 cross_references EMBL,GenBank, NID: 9415383; FID: 9415384
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ENTRY          C21056      *type fragment
TITLE          kappa chain precursor V region (H137) - human (Tzeng et al.)
AUTHOR        Otsuka, Tame Homo sapiens (common name man)
DATE          20-Mar-1998 sequence-version 0; Aug-1990 text-change
ACCESSIONS    REFERENCE   C21055
                D.L.; Rabbitts, T.H.
                Cell 10(93), 12,181-187, 1983
                Evolution of immunoglobulin V genes: evidence indicating that
                recently duplicated human V-kappa sequences have diverged
                *across-reference MID 8329350n.
ACCESSION     C21055
STATUS        preliminary
**status      **type       L117 **label NEW
**reference   **sequence DB-000246: MID-8185991; PID-9185992
CLASSIFICATION superfamily Immunoglobulin V region; immunoglobulin homology
INTERESTED PARTY interested party: immunoglobulin
SYNOPSIS      length 111; conserved 704
Query Match   11:0% score 16; DB 2; length 117;
               Pct Identical 16; Pct Diff 2,6;e-18;
Matched       Conservative 0; Mismatches 0; Indels 0; gaps 0;
DB             21 ACTION=PPSI:PLANS 36
```

[illegible]

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#accession S21668
#molecule-type DNA
#residues 1-117 #label ROE
#cross-references EMBL:X6643; NID:q43263; PID:e45457; PID:g335151
#superfamily Immunoglobulin V region: Immunoglobulin homology
#keywords heterotrimer; Immunoglobulin
#summary $length 117 $molecular-weight 12656 $checksum 7496

Query Match
Best Local Similarity 100.0% Pred. No. 2.61e-18
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 RCDIONSPSSISAS 36
QY 19 RCDIONSPSSISAS 34

RESULT 42
#accession S24306
#molecule-type DNA
#residues 1-117 #label PAM
#cross-references EMBL:X59315; NID:g33252; PID:g33256
#superfamily Immunoglobulin V region: Immunoglobulin homology
#keywords heterotrimer; Immunoglobulin
#summary $length 117 $molecular-weight 12656 $checksum 7496

Query Match
Best Local Similarity 100.0% Pred. No. 2.61e-18
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 RCDIONSPSSISAS 36
QY 19 RCDIONSPSSISAS 34

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CLASSIFICATION #superfamily Immunoglobulin V region: Immunoglobulin homology
#keywords heterotrimer; Immunoglobulin
#summary $length 117 $molecular-weight 12656 $checksum 7496

Query Match
Best Local Similarity 100.0% Pred. No. 2.61e-18
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 RCDIONSPSSISAS 36
QY 19 RCDIONSPSSISAS 34

RESULT 44
#accession S46370
#molecule-type DNA
#residues 1-117 #label BEN
#cross-references EMBL:X6640; NID:q43264; PID:e45455; PID:g335149
#superfamily Immunoglobulin V region: Immunoglobulin homology
#keywords heterotrimer; Immunoglobulin
#summary $length 117 $molecular-weight 12656 $checksum 7496

Query Match
Best Local Similarity 100.0% Pred. No. 2.61e-18
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 RCDIONSPSSISAS 36
QY 19 RCDIONSPSSISAS 34

```

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CLASSIFICATION #superfamily Immunoglobulin V region: Immunoglobulin homology
#keywords heterotrimer; Immunoglobulin
#summary $length 117 $molecular-weight 12656 $checksum 7496

Query Match
Best Local Similarity 100.0% Pred. No. 2.61e-18
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 RCDIONSPSSISAS 36
QY 19 RCDIONSPSSISAS 34

RESULT 43
#accession K10561
#molecule-type DNA
#residues 1-117 #label BEN
#cross-references EMBL:X6640; NID:q43264; PID:e45455; PID:g335149
#superfamily Immunoglobulin V region: Immunoglobulin homology
#keywords heterotrimer; Immunoglobulin
#summary $length 117 $molecular-weight 12656 $checksum 7496

Query Match
Best Local Similarity 100.0% Pred. No. 2.61e-18
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 RCDIONSPSSISAS 36
QY 19 RCDIONSPSSISAS 34

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```

CLASSIFICATION #superfamily Immunoglobulin V region: Immunoglobulin homology
#keywords heterotrimer; Immunoglobulin
#summary $length 117 $molecular-weight 12656 $checksum 7496

Query Match
Best Local Similarity 100.0% Pred. No. 2.61e-18
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 RCDIONSPSSISAS 36
QY 19 RCDIONSPSSISAS 34

RESULT 46
#accession S21667
#molecule-type DNA
#residues 1-117 #label ROE
#cross-references EMBL:X6640; NID:q43264; PID:e45455; PID:g335151
#superfamily Immunoglobulin V region: Immunoglobulin homology
#keywords heterotrimer; Immunoglobulin
#summary $length 117 $molecular-weight 12656 $checksum 7496

Query Match
Best Local Similarity 100.0% Pred. No. 2.61e-18
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 RCDIONSPSSISAS 36
QY 19 RCDIONSPSSISAS 34

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Best Local Similarity 100.0% Pred. No. 2 Size 10:
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 24 RCDIOMTSPSSISLS 39
CY 19 RCDIOMTSPSSISLS 34

RESULT 47
ENTRY 540314 *type complete
TITLE 1g kappa chain V region: immunoglobulin homology
ORGANISM Homo sapiens
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change
ACCESSIONS 540312
REFERENCE Klein, R.; Jaenichen, R.; Zachau, H.G.
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expression of human immunoglobulin chl genes and their
#accession 540314
#status preliminary; translation not shown
#molecule-type mRNA #label KLE
#cross-references EMBL:X72423
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology
REMARKS heterotrimer: immunoglobulin
SDMARY length 123 molecular-weight 13196 #checksum 765

Query Match 11.0% Score 16; DB 2; Length 123:
Best Local Similarity 100.0% Pred. No. 2 Size 10:
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 14 RCDIOMTSPSSISLS 29
CY 19 RCDIOMTSPSSISLS 34

RESULT 48
ENTRY 540331 *type complete
TITLE 1g kappa chain - human
ORGANISM Homo sapiens
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change
ACCESSIONS 540332
REFERENCE Klein, R.; Jaenichen, R.; Zachau, H.G.
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expression of human immunoglobulin chl genes and their
#accession 540331
#status preliminary; translation not shown
#molecule-type mRNA #label KLE
#cross-references EMBL:X72423
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology
REMARKS heterotrimer: immunoglobulin
SDMARY length 123 molecular-weight 13401 #checksum 9338

Query Match 11.0% Score 16; DB 2; Length 123:
Best Local Similarity 100.0% Pred. No. 2 Size 10:
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 15 RCDIOMTSPSSISLS 30
CY 19 RCDIOMTSPSSISLS 34

RESULT 50
ENTRY 503521 *type fragment
TITLE 1g kappa chain precursor V region (hybridoma PFR-02) - mouse
ORGANISM Mus musculus
DATE 08-Sep-1997
ACCESSIONS 503521
REFERENCE Adzhahov, V.A.; Stepanenko, A.G.; Deery, S.A.; Polymovskii, O.L.
#authors Adzhahov, V.A.; Stepanenko, A.G.; Deery, S.A.; Polymovskii, O.L.
#journal Mol. Biol. (1987) 21:945-949
#title Structure of the variable gene coding for chl-chains of
#accession 503521
#molecule-type DNA
#cross-references EMBL:X07953; NID:933645; PID:933646
GENETICS 17/3
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology
REMARKS heterotrimer: immunoglobulin
SDMARY length 124 #checksum 9886

Query Match 11.0% Score 16; DB 2; Length 124:
Best Local Similarity 100.0% Pred. No. 2 Size 10:
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 18 DIONOTSPSSISLS 33
CY 21 DIONOTSPSSISLS 36

ORGANISM Mus musculus
DATE 08-Sep-1997
ACCESSIONS 503521
REFERENCE Adzhahov, V.A.; Stepanenko, A.G.; Deery, S.A.; Polymovskii, O.L.
#authors Adzhahov, V.A.; Stepanenko, A.G.; Deery, S.A.; Polymovskii, O.L.
#journal Mol. Biol. (1987) 21:945-949
#title Structure of the variable gene coding for chl-chains of
#accession 503521
#molecule-type DNA
#cross-references EMBL:X07953; NID:933645; PID:933646
GENETICS 17/3
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology
REMARKS heterotrimer: immunoglobulin
SDMARY length 124 #checksum 9886

Query Match 11.0% Score 16; DB 2; Length 124:
Best Local Similarity 100.0% Pred. No. 2 Size 10:
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 18 DIONOTSPSSISLS 33
CY 21 DIONOTSPSSISLS 36

Best Local Similarity 100.0% Pred. No. 2 Size 10:
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 24 RCDIOMTSPSSISLS 39
CY 19 RCDIOMTSPSSISLS 34

RESULT 47
ENTRY 540314 *type complete
TITLE 1g kappa chain V region: immunoglobulin homology
ORGANISM Homo sapiens
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change
ACCESSIONS 540312
REFERENCE Klein, R.; Jaenichen, R.; Zachau, H.G.
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expression of human immunoglobulin chl genes and their
#accession 540314
#status preliminary; translation not shown
#molecule-type mRNA #label KLE
#cross-references EMBL:X72423
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology
REMARKS heterotrimer: immunoglobulin
SDMARY length 123 molecular-weight 13196 #checksum 765

Query Match 11.0% Score 16; DB 2; Length 123:
Best Local Similarity 100.0% Pred. No. 2 Size 10:
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 14 RCDIOMTSPSSISLS 29
CY 19 RCDIOMTSPSSISLS 34

RESULT 48
ENTRY 540331 *type complete
TITLE 1g kappa chain - human
ORGANISM Homo sapiens
DATE 06-Mar-1994 #sequence_revision 26-May-1995 #text_change
ACCESSIONS 540332
REFERENCE Klein, R.; Jaenichen, R.; Zachau, H.G.
#authors Klein, R.; Jaenichen, R.; Zachau, H.G.
#journal Eur. J. Immunol. (1993) 23:3248-3271
#title Expression of human immunoglobulin chl genes and their
#accession 540331
#status preliminary; translation not shown
#molecule-type mRNA #label KLE
#cross-references EMBL:X72423
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology
REMARKS heterotrimer: immunoglobulin
SDMARY length 123 molecular-weight 13401 #checksum 9338

Query Match 11.0% Score 16; DB 2; Length 123:
Best Local Similarity 100.0% Pred. No. 2 Size 10:
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 15 RCDIOMTSPSSISLS 30
CY 19 RCDIOMTSPSSISLS 34

RESULT 50
ENTRY 503521 *type fragment
TITLE 1g kappa chain precursor V region (hybridoma PFR-02) - mouse
ORGANISM Mus musculus
DATE 08-Sep-1997
ACCESSIONS 503521
REFERENCE Adzhahov, V.A.; Stepanenko, A.G.; Deery, S.A.; Polymovskii, O.L.
#authors Adzhahov, V.A.; Stepanenko, A.G.; Deery, S.A.; Polymovskii, O.L.
#journal Mol. Biol. (1987) 21:945-949
#title Structure of the variable gene coding for chl-chains of
#accession 503521
#molecule-type DNA
#cross-references EMBL:X07953; NID:933645; PID:933646
GENETICS 17/3
CLASSIFICATION Superfamily immunoglobulin V region: immunoglobulin homology
REMARKS heterotrimer: immunoglobulin
SDMARY length 124 #checksum 9886

Query Match 11.0% Score 16; DB 2; Length 124:
Best Local Similarity 100.0% Pred. No. 2 Size 10:
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 18 DIONOTSPSSISLS 33
CY 21 DIONOTSPSSISLS 36

!!SEQUENCE LIST 1.0

(Peptide) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-2 check: 4259 from: 1

FROMIG of: /home/obryen/ree455/olig/us08836455.pep
sequence 2, application us/08836455

general information:

applicant: chatterjee, malaya
applicant: loon, kenneth a.
applicant: chatterjee, sunil k. . .

TO: geneseqp: * Sequences: 162,890 Total-length: 20,225,328 April 18, 1999 14:35

Database Release Information:

Genesep-AA, Release 34.4, Released on 4Feb1999, Formatted on 5Feb1999

Word-size: 5 Words: 56705 Diagonals: 5,617 Total-diagonals: 43,681,344
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 5.25

Sequence Stnd Diag Score Width Documentation ..

GENESOP:W27119	+	0	145	1	Murine monoclonal anti-Idiotypic anti-
GENESOP:P30251	+	2	129	1	Sequence of the leader, variable regi
GENESOP:R39559	+	113	100	1	Sequence of 520C9 sFV protein. New s
GENESOP:W02280	+	113	100	1	520C9 anti-c-erbB-2 two single chain
GENESOP:W04244	+	113	100	1	520C9 sFV sequence. Nucleic acid enc
GENESOP:W53170	+	113	100	1	520C9 anti-c-erbB-2 sFV' dimeric cons
GENESOP:W27121	+	404	96	1	Murine antibody light chain variable
GENESOP:R39571	+	404	94	1	Sequence of G-Fit. New single chain F
GENESOP:R21310	+	20	93	1	Light chain of Mif clone. Producing m
GENESOP:W18271	+	20	88	1	Prp 37 light chain variable region. N
GENESOP:W22537	+	2	85	1	Murine anti-human class II monoclonal
GENESOP:R79250	+	20	84	1	Light chain variable region for monoc
GENESOP:R79247	+	20	84	1	Light chain variable region for monoc
GENESOP:R82030	+	20	83	1	Light chain variable region for monoc
GENESOP:W18270	+	20	75	1	Light chain variable region of murine
GENESOP:R21286	+	20	71	1	Prp 28 light chain variable region. N
GENESOP:W18269	+	20	63	2	Murine VL kappa group V chain "a", sp
GENESOP:W27089	+	20	63	1	Prp 81 light chain variable region. N
GENESOP:W27088	+	20	60	1	Murine monoclonal antibody B9 light ch
GENESOP:R89686	+	0	56	1	Anti-Idiotypic antibody 3H1 light cha
GENESOP:R88410	+	0	56	1	Monoclonal anti-Idiotypic antibody 3H1
GENESOP:R28670	+	0	54	1	3H1 light chain variable region. Recd
GENESOP:R39265	+	0	54	1	PPM-X3 protein product. Reconstituted
GENESOP:W15935	+	20	54	1	Mouse C4G1 Ig light-chain. Compn. cc
GENESOP:W10233	+	20	53	1	Antibody 3G2 light chain variable reg
GENESOP:R52040	+	20	53	1	Variable region of mouse antibody C4G
GENESOP:R15322	+	20	53	1	Light chain variable region of human
GENESOP:R84553	+	0	52	1	TF8-5G9 CDR-grafted light chain. CDR-
GENESOP:W11918	+	0	52	1	IL-2 chimeric antibody light chain. N
GENESOP:W70954	+	0	52	1	MAB SCH94.03 light chain. Monoclonal
GENESOP:R15321	+	0	51	1	Murine MAB SK48-R26 light chain. Recd
GENESOP:R62881	+	0	50	1	Light chain of monoclonal antibody R5
GENESOP:R09426	+	0	49	1	IL-2 chimeric antibody light chain. N
GENESOP:R32121	+	0	49	1	Murine anti-human atherosclerotic pla
GENESOP:W06215	+	0	49	1	ME4 Light Chain V Region (mouse). Ch
GENESOP:R29010	+	0	49	1	Anti-CD4 antibody M7 15.1 light chain
GENESOP:W16620	+	0	48	1	MAB ME4 light chain variable region.
GENESOP:W11815	+	20	47	1	p146-K3 protein product. Reconstitute
GENESOP:W04177	+	20	47	1	Anti-human Fas ligand antibody (NOK1) light
GENESOP:W60033	+	0	47	1	Mouse anti-human Fas ligand antibody
GENESOP:R53803	+	21	46	2	Variant variable light chain of Fas l
GENESOP:W35125	+	20	46	1	Mouse antibody F919-9-18 light chain
GENESOP:W35130	+	20	46	1	FAB light chain for F19.9. New ligand
GENESOP:W35129	+	98	46	1	R. piplens recombinant RNase ronc fus
GENESOP:W35127	+	98	46	1	R. piplens recombinant RNase ronc fus
GENESOP:W35126	+	122	46	1	R. piplens recombinant RNase ronc fus
GENESOP:W35128	+	100	46	1	R. piplens recombinant RNase ronc fus

5 amino acids long

of 490. Containing matches at least

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CC Comparing cluster of antigen-targeting antibody fragment constructs
 CC Example 1: columns 33-36: 30pp: English
 CC Variable heavy (VH) and variable light (VL) genes were cloned from
 CC a 2009 hybridoma cDNA library, using probes directed toward the
 CC variable regions of the heavy and light chain genes, respectively.
 CC The variable regions of the heavy and light chain genes were
 CC joined by PCR to create a single chain (scFv) gene.
 CC The scFv gene was constructed by connecting the VH and VL genes
 CC with a flexible linker. The resulting 52009 two scFv genes,
 CC which encode the present sequence, were inserted into an expression
 CC vector. The expression vector was then transfected into a cell
 CC line, resulting in the production of the scFv protein.
 CC The scFv protein was purified by ion exchange chromatography
 CC and used for in vivo imaging, and drug targeting experiments. The
 CC scFv protein was used as a homodimer, in which both fragments target
 CC the same antigen. The scFv protein was used for in vivo imaging and
 CC longer tissue retention times, compared to individual scFv protein
 CC fragments.

Query Match 20.0% Score 29: DB 18: Length 243:
 Best Local Similarity 100.0%: Pred. No. 9,986-26:
 Matches 29: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 189 apyrtfgrsgdyalttsleedrv 217
 76 SCVPRSGSGSDYSLTISLEEDRV 104

RESULT 8
 ID R39569 standard: Protein: 246 AA.
 AC R39569: 246
 DE 07-FEB-1994 (first entry)
 KW Single chain Fv polypeptide: VH-VL heterodimer; immunoglobulin; Ig;
 KW bioengineered single polypeptide chain binding site; aa.
 OS Synthetic.
 PE 05-FEB-1993: 001055.
 PR 06-FEB-1993: 001055.
 PA (CENTU) CENTU ONCOLOGY CORP.
 PI Houston TX, Huston JS, Oppermann H, Ring DB;
 DR N-PSDB: Q46084.
 CC The single chain Fv polypeptide binding to C-erbB-2 tumour
 CC antigen, for imaging or treating breast or ovarian cancer etc.
 CC Claim 4: pages 60-61: 87pp: English.
 CC C-erbB-2 refers to a protein antigen expressed on the surface of
 CC tumour cells, such as breast and ovarian tumour cells, which is an
 CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric

OY 76 SCVPRSGSGSDYSLTISLEEDRV 104

RESULT 10
 ID P93035 standard: Protein: 213 AA.
 AC P93035: 213
 DE 14-MAR-1990 (first entry)
 KW Chimeric antibody light chain variable region.
 KW chimeric antibody; light chain variable region.
 OS Synthetic.
 PE 05-FEB-1993: 001055.
 PR 06-FEB-1993: 001055.
 PA (CENTU) CENTU ONCOLOGY CORP.
 PI Houston TX, Huston JS, Oppermann H, Ring DB;
 DR N-PSDB: Q46084.
 CC The single chain Fv polypeptide binding to C-erbB-2 tumour
 CC antigen, for imaging or treating breast or ovarian cancer etc.
 CC Claim 4: pages 60-61: 87pp: English.
 CC C-erbB-2 refers to a protein antigen expressed on the surface of
 CC tumour cells, such as breast and ovarian tumour cells, which is an
 CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric

Query Match 19.3% Score 28: DB 1: Length 213:
 Best Local Similarity 100.0%: Pred. No. 1,986-24:
 Matches 28: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 94 pttgggkrlkrdapvslfppas 121
 115 pttgggkrlkrdapvslfppas 142

RESULT 11
 ID W27089 standard: Protein: 214 AA.
 AC W27089: 214
 DE 18-NOV-1997 (first entry)
 KW House monoclonal antibody B9 light chain.
 KW house monoclonal antibody; light chain.
 KW antibody; B9.
 OS Mus musculus.
 PE 05-FEB-1993: 001055.
 PR 06-FEB-1993: 001055.
 PA (CENTU) CENTU ONCOLOGY CORP.
 PI Houston TX, Huston JS, Oppermann H, Ring DB;
 DR N-PSDB: Q46084.
 CC The single chain Fv polypeptide binding to C-erbB-2 tumour
 CC antigen, for imaging or treating breast or ovarian cancer etc.
 CC Claim 4: pages 60-61: 87pp: English.
 CC C-erbB-2 refers to a protein antigen expressed on the surface of
 CC tumour cells, such as breast and ovarian tumour cells, which is an
 CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric

CC pt. of about 5.3 (see Q46083, R39568). A single chain Fv (scFv)
 CC is a covalently linked VH-VL heterodimer which is expressed from
 CC a gene construct including VH- and VL-encoding genes connected by
 CC a flexible linker. The scFv gene was constructed by connecting the
 CC variable regions of the heavy and light chain genes, respectively.
 CC The variable regions of the heavy and light chain genes were
 CC joined by PCR to create a single chain (scFv) gene.
 CC The scFv gene was constructed by connecting the VH and VL genes
 CC with a flexible linker. The resulting 52009 two scFv genes,
 CC which encode the present sequence, were inserted into an expression
 CC vector. The expression vector was then transfected into a cell
 CC line, resulting in the production of the scFv protein.
 CC The scFv protein was purified by ion exchange chromatography
 CC and used for in vivo imaging, and drug targeting experiments. The
 CC scFv protein was used as a homodimer, in which both fragments target
 CC the same antigen. The scFv protein was used for in vivo imaging and
 CC longer tissue retention times, compared to individual scFv protein
 CC fragments.

Query Match 20.0% Score 29: DB 8: Length 246:
 Best Local Similarity 100.0%: Pred. No. 9,986-26:
 Matches 29: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 189 apyrtfgrsgdyalttsleedrv 217
 76 SCVPRSGSGSDYSLTISLEEDRV 104

RESULT 6
 ID R39571 standard: Protein: 534 AA.
 AC R39571: 534
 DE 07-FEB-1994 (first entry)
 KW Sequence of c-erbB-2, c-erbB-3, c-erbB-4.
 KW Synthetic antigen; c-erbB-2, c-erbB-3, c-erbB-4.
 OS Synthetic.
 PE 05-FEB-1993: 001055.
 PR 06-FEB-1993: 001055.
 PA (CENTU) CENTU ONCOLOGY CORP.
 PI Houston TX, Huston JS, Oppermann H, Ring DB;
 DR N-PSDB: Q46084.
 CC The single chain Fv polypeptide binding to C-erbB-2 tumour
 CC antigen, for imaging or treating breast or ovarian cancer etc.
 CC Example: pages 65-68: 87pp: English.
 CC Claim 4: pages 60-61: 87pp: English.
 CC C-erbB-2 refers to a protein antigen expressed on the surface of
 CC tumour cells, such as breast and ovarian tumour cells, which is an
 CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
 CC pt. of about 5.3 (see Q46083, R39568).

Query Match 20.0% Score 29: DB 8: Length 534:
 Best Local Similarity 100.0%: Pred. No. 9,986-26:
 Matches 29: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 480 apyrtfgrsgdyalttsleedrv 508
 115 pttgggkrlkrdapvslfppas 142

FT region 108..214
 PA 109154587-A. /label= Cxappa
 PD 17-JUN-1997.
 PE 09-MAY-1996: 114492.
 PR 02-NOV-1995: KR-039459.
 DR N-PSDB: 285091.
 CC The present sequence represents the mouse monoclonal antibody B9 light
 CC chain (B9L), which binds specifically to human blood apolipoprotein
 CC B-100. The nucleic acid can be used in a method for the preparation
 CC of a recombinant antibody which specifically binds human plasma
 CC determining the concentration of human plasma apolipoprotein B-100
 CC in a sample. The antibody is also useful in a drug composition for
 CC plasma apolipoprotein B-100.
 CC Sequence 214 AA:
 Query Match 19.3% Score 28: DB 24: Length 214:
 Best Local Similarity 100.0%: Pred. No. 1,986-24:
 Matches 28: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 95 pttgggkrlkrdapvslfppas 122
 115 pttgggkrlkrdapvslfppas 142

RESULT 12
 ID W19935 standard: Protein: 216 AA.
 AC W19935: 216
 DE 09-JUN-1997 (first entry)
 KW Antibody 362 light chain variable region.
 KW catalytic antibody; antioleosteric hydrolysis; hydrolase.
 KW ZAA7612: ZAA7612: ds.
 OS misc.
 PE 05-FEB-1993: 001055.
 PR 06-FEB-1993: 001055.
 PA (CENTU) CENTU ONCOLOGY CORP.
 PI Houston TX, Huston JS, Oppermann H, Ring DB;
 DR N-PSDB: Q46084.
 CC The single chain Fv polypeptide binding to C-erbB-2 tumour
 CC antigen, for imaging or treating breast or ovarian cancer etc.
 CC Claim 4: pages 60-61: 87pp: English.
 CC C-erbB-2 refers to a protein antigen expressed on the surface of
 CC tumour cells, such as breast and ovarian tumour cells, which is an
 CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric

Machine	37:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps
Db	127	127	127	127	127	127	127	127
0y	118	118	118	118	118	118	118	118
RESULT	21							
ID	R40385	standard: Protein: 225 AA.						
AC	R40385:							
DR	08-FEB-1994	(first entry)						
DE	Monoclonal antibody (Ma2pa) 2,3 light chain: light chain:							
FM	2,3 light chain: light chain:							
FW	Immunoglobulin: bispecific Bivalent antibody: cell-targeting:							
FN	cytoxic agent.							
FT	Key	Location/Qualifiers						
FT	peptide	/label= signal_peptide						
FT	region	13..118						
FT	region	/label= variable						
FT	region	119..125						
FT	region	/label= constant						
PN	EP-55611-A.							
PD	18-AUG-1993.							
PF	08-FEB-1993.	400323						
PI	18-AUG-1993.	0020505.						
PA	(BOUL/ BOULAIN J							
PA	(COMS/ COMMISSARINAE ENERGIE ATOMIQUE.							
PI	BOULAIN J, DUCANES F, GILLET D, MENES A;							
PI	N-TERM. 046038.							
PT	New immunoglobulin hybrid proteins - with immunoglobulin							
PT	fragments linked to dimeric protein, for diagnostic or							
PS	therapeutic uses 3370p. [Rev.]							
CC	A fragment of the heavy chain (VH + CH) from the anti-rat small							
CC	neurotoxin monoclonal antibody (Ma2pa)2,3 was PCR-amplified from							
CC	hybridoma-derived cDNA using primers Q46039 and Q46040. A light							
CC	primer Q46041 and Q46042. The two amplicon fragments were using							
CC	inserted into the same vector: the H-chain fragment was inserted							
CC	(in-frame) between codons 6-7 of the phoA coding sequence and the							
CC	phoA 8' sequence was added. The first 6 codons of the phoA							
CC	gene were deleted. The resulting construct was transformed into							
CC	the terminator termination sequence of phoA. The fusion							
CC	protein was purified and the first 6 codons of the phoA							
CC	gene were deleted. The resulting construct was transformed into							
CC	identical Ab-derived units. The fusion hybrid protein, comprising two							
CC	proteins containing two different Ab-derived units (1.e. to produce							
CC	bispecific antibodies). When a toxic protein is used in place of							
CC	phoA, the hybrid molecules can be used as cell-targeting							

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CC therapeutic agents.
SQ sequence      225 AA;
Query March          18 f6; Score 27; DB #; Length 225;
Best Local Similarity 100.0%; Pident No. 3 Epe-23;
Matches    27; Conservative   0; Mismatches 0; Indels   0; Gaps 0;
Db         116 yf9qgahhhhhhhhhaapppppps     133
              |||||.....||||..|||.
OY        116 YPGCGLEELKNNALAPVPSIFPPSS 142


RESULT_22
ID R12B6 standard protein; 108 AA.
AC R12B6.
DT 21-MAY-1993 (date entry)
DR Protein Data Bank, Geneva, CH; SwissProt database;
PR Primary source: cDNA clone; tissue: rat pituitary gland;
PM PubMed; gfp binding; adaptation: gene VIII; diverse receptor;
KW specific binding pattern; replicable genetic display package.
OS Synthetic.
PE Binding_site location/qualifiers
PT 21-34 /label=CDR1
FT binding_site 50..56
FZ 6A96G - CDR2
FT binding _site /label=CDR3
FT D-X-C-Y-X motif *
WQ92JN042.4.
PR 10-JUL-1993; GOL134.
PR 10-JUL-1990; GB-015198.
PR 13-OCT-1980; GB-012843.
PR 14-FEB-1993; GB-009744.
PR 06-MAR-1993; GB-004744.
PR 15-MAY-1993; GS-010549.
PA (CAND1)- CANDIDE ANTIBODY.
NC NCBI GENES CONNECT.
PI Jackson RH, Connolly JO, Johnson ES, Hoogenboom HR, Griffiths AD;
P1 Walter GP, Bonnett TP;
P2 WPL 91-0568E/207 of specific binding pHis - by expression in
P3 recombinant host cells with a secretory replicable genetic
P4 display package.
P5 Example 21; Fig 24; 20ppr English.
P6 Kramarz SJ, Huse DM, Wilson JH, Lippert JR (1986-93) found to be expressed
P7 from a single chain Tc library from an immunized mouse. The libra-
P8 ry produces a diverse repertoire of antibody fragments specific for
P9 2-pmpyri-5-carotoline (pMX). It was prep'd using CDNA generated
```

CC from mA from mice immunized with phox coupled to elicited serum
CC albumin. The vHc and Vh kappa sequences were separately amplified
CC by PCR using Q23V9-98 and ligated into pTZ191 for ex-
CC pression in E. coli. The resulting library was screened with the
CC rat library of clones was derived. Twenty three B-cell binding
CC R1266-17) in a variety of pairings with the seven different Vh
CC genes (4-9). Of the twenty three clones sequenced, three were of
CC genes (4-9), while the other nine were of genes (10-13). Mature JH
CC (JH1-18, 1985) were also sequenced. The results are shown in
CC Figure 1. The results show that the sequence of the Vh gene
CC gly or which is needed to create a cavity for phox. Most of the
CC clones were Vh-d combinations. The Rd of Vh/dX/d for phox-GABA
CC was 10 nM. Only two other combinations (of eleven tested) were
CC found to have higher values. This suggests that phage bearing sepe
CC bably due to the avidity of the multiple antibody heads on the
CC phage.
CC See also R12660-307, 309-311; R23450, 565-581.
CC Sequence 108 MA.

```

Query Match      17.9%  Score 76  DB 4:  Length 108:
      Similarity 100.0%  P-Id No. 7,35e-21
      Best Local 100.0%  P-Id No. 7,35e-21
Matched  50  Conservative  0  Mismatches  0  Indels  0  Gaps  0
Db      56  acbmtb1rsgsacdbiol1:aa1eae  81
76  scvrttssgssbndyct1:iss1sae  101
Q7

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23 RESULT 23
 ID R3307: standard; protein; 126 AA.
 DC R3307: 1993 (file entry)
 DE MELL1 light chain
 RN Antibody; high affinity; FCER2; low affinity; FCER1;
 RM 19E receptor; histamine; mast cell; Anaphyl; Rabbit;
 KW CDR; mutase; MELL1; MARI3; MARI5; MARI7.
 OS Synthetic.
 OS WO9304113A.
 PR 14-MAR-1993.
 PR 14-MAR-1993: US-744760.
 PR 07-MAY-1993: US-879493.
 PA (GENTH) GENENTECH INC.
 PI JARDIN PR, Presta LD.
 PI 14-MAR-1993: 11.
 PT 19E antibody; binding to specific Fc epsilon receptors - act as
 PT 19E antibodies; useful for treating and preventing 19E-mediated
 PT disorders e.g. allergies.
 PT Antibodies: Fig 2; 11pp: English.
 CC Antibodies capable of binding FCER2-bound 19E but which are

[illegible]

RESULT	24
AD	R19322 standard Protein: 144 AA.
AE	R19322
AF	R19322
AG	IL-2-IL-2R-1992 (first entry)
DE	IL-2-chimeric antibody light chain.
DM	Interleukin-2; immunosuppressant.
DN	Interleukin-2; immunosuppressant.
OS	Chimeric heavy antigen
PR	Key
PT	peptide
PT	1..20
PT	/notes="signal peptide"
PT	peptide
PT	/notes="V-region"
PT	peptide
PT	116..127
PT	/notes="J1-region"
PT	peptide
PT	128..130
PT	/notes="C-region"
PN	EP-460674-A.
PD	11-DEC-1991
PD	109103
PR	08-JUN-1990; DE-018442.
PA	(BOER) BOEHRINGER MANNHEIM GMBH.
PI	Weidle U, Kallaua B, Knapp W.
DR	W-8093; 031118/50.
PT	New recombinant DNA encoding chimeric antibody - with human
PT	constant and non-human variable regions, esp. directed against
PT	interleukin 2 receptor (4pp, German).
PT	11-DEC-1991
CC	The sequence is that of interleukin-2 (IL-2) chimeric antibody
CC	light chain, coded by clone 447. Antibodies against IL-2 receptors
CC	are useful as immunosuppressants, and are much less immunogenic than
CC	sequence 144 AA.
CC	sequence 144 AA.

[illegible]

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RESULT	37
AD	R18169 standard; Protein; 112 MA.
DZ	14-FEB-1992 (first entry)
DZ	86-S-06 anti-ICAM-1 light chain.
NM	Intercellular adhesion molecule-1; antibody; chimeric.
PM	Key molecules.
PT	peptide
PT	Location/Qualifiers
PT	1..193
PT	/label=signal_sequence
PT	peptide
PT	1..193
PT	/note="confirmed by N-terminal analysis"
PT	43..58
PT	/label=CDR
PT	region
PT	44..60
PT	/label=CDR
PT	region
PT	113..121
PT	/label=CDR
PT	133..172
PT	/label=constant_domain
PN	W01161626-N.
PD	14-NOV-1991
PR	622946
PR	27-APR-1990; CH 4556.
PA	(CELL-) CELLTECH LTD.
PA	(BOEY) BOEHRINGER INGELHEIM PHA.
DR	MOLYT, JR., ROHLINGEN SM, ROTHLEIN RA;
DR	N-PSDB: Q16551.
PT	New humanised chimeric anti-ICAM-1 antibodies - useful in treating inflammation e.g. psoriasis and ulcerative colitis to disrupt metastasis of haemopoietic tumour cells and in Diagnostics; Fig 1; 65pp; English.
CC	The sequence comprises the amino sequence, variable region and part of the constant region of the 86-S-06 murine Ab light chain. The hybridoma cell line 86-S-06 was deposited with the European Patent Office by Boehringer Ingelheim Pharmaceuticals Inc. The cells were provided as a gift to the University of Oxford and used to prepare cDNA for a library in pSP64 and mRNA isolated and used to prepare cDNA for a library in pSP64 screened using a probe complementary to the heavy chain. A cDNA library was grown in E. coli HB101 and colonies kepta containing region or with a 980 bp BamHI-XbaI restriction fragment of a previously isolated mouse IgG2a constant region clone. From the second round of screening, positive clones were selected from the second round of screening. The DNA was sequenced. The protein sequence was deduced from the DNA. The Ab was used to construct humanised Abs having chimeric variable regions, i.e. with a constant region domain. The Abs can be used to treat inflammation, to suppress metastasis of haemopoietic tumour

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17 100% Monoclonal anti-idiotypic antibodies matching epidermal growth
18 factor.
19 CC Claim 6, p45-50: 28p11. Bands
20 CC Marine monoclonal anti-idiotypic antibodies, 1988, 386 and 586 are
21 CC new. They induce an immune response against epidermal growth factor
22 CC regions of 178k, are sequences of the heavy and light chain variable
23 CC antibodies are used for the manufacture of drugs against the
24 CC tumours that express EGFR on their surface, including melanoma,
25 CC glioma and carcinoma.
26 Sequence 146 MA.
27
28 Query Match 17.9% Score 26; DB 22; Length 146;
29 Best Local Similarity 100.0%; Pstd. No. 7.53e-22;
30 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0
31
32 Db 119 ytfgggghlrlhrdadpavtstppss 144
33 |||||
34 116 ytfgggghlrlhrdadpavtstppss 141
35
36 RESULT 26
37 ID P91078 standard; peptide: 148 MA.
38 DT 14-NOV-1990 (first entry)
39 DT Light chain of monoclonal antibody 6A4.
40 NM Monoclonal antibody 6A4; light chain; Pseudomonas aeruginosa; OMP-1.
41 CA 3-383935-5A.
42 PR 13-APR-1989; 106463.
43 PR 15-APR-1989; DE-811023.
44 PR (EMV) Bahringer et al.
45 PR WPMR 1, 11986-1987.
46 DR N-PDB: 193663
47 DR N-PDB: 193663
48 F2 Monoclonal antibody to Pseudomonas aeruginosa - and DNA coding for
49 F2 variable antibody regions.
50 CC 1989, 999. German
51 CC The peptide is encoded by the light chain of monoclonal antibody 6A4.
52 CC 6A4 reacts with the OMP-1 protein of all 19 known serotypes of
53 CC Pseudomonas. It is used for therapy and diagnosis of infection, and
54 CC as carrier for drugs. The antibody is IgG2a subclass.
55 Sequence 148 MA.
56
57 Query Match 17.9% Score 26; DB 1; Length 148;
58 Best Local Similarity 100.0%; Pstd. No. 7.53e-22;
59 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
60
61 Db 122 tfgggghlrlhrdadpavtstppss 147
62 |||||
63 117 tfgggghlrlhrdadpavtstppss 142

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	Conservative	Mismatches	Indels	Gaps
D _B 56 <i>scvppitgssagdaatlaals</i> 80 QY 76 <i>scvpprrsgssgsdysltlslls</i> 100	0:	0:	0:	0

ABSTRACT 37	PROCEEDINGS
R99686 standard; Protein; 142 kDa.	NC
R99686;	NC
11-OCT-1996 (first entry)	NC
Monoclonal anti-idiotypic antibody JH1 light chain variable region	DE
Anti-idiotypic antibody; monoclonal antibody; CEA;	DE
carcinoembryonic antigen; tumour-associated antigen; cancer;	DE
vaccine; immunotherapy.	DE

RESULT	41	standard: peptide: 153 AA.
AD	817207	
DE	23-MOV-1995	(first entry)
DR	Mouse monoclonal antibody 1668	light chain sequence derived from
DS	CDM.	
OS	synthetic	
PM	MO316038-A.	
PR	15-DIV-1995.	
PR	08-IND-1994.	1B0387.
PA	(MERC)/MERCER C P	
PA	(TCEL-) T CEL SCI INC.	
PA	LN AV	
DE	15-24122/29.	specific for select sub-population of T cells
PT	useful for treatment of Crohn disease	
PS	Diagnosis: Page 63: 92pp: English.	
PS	A mouse monoclonal antibody (mab), 1668, which recognizes human V	
CC	framework region immunized by CDR grafting certain CDR and select	
CC	REI light chain transmembrane	
CC	heavy (IgG1) and light (L) chains in mammalian cell fusion	
CC	vectors with Neo and DHFR selection markers, respectively, were	
CC	followed by into a DHFR-Chinese hamster fibroblast (CHO) cell line	
CC	selected designated "M29" transfection. The humanised MAb that was	
CC	TCR V beta 8.1. It is used as a therapeutic agent for	
CC	Crohn's disease.	
CC	sequence: 153 AA:	
Query Match	15.24;	Score 22; DB 11; Length 153;
Best Local Similarity	100.00;	Peed. No. 9,59e-17;
Matches	21; Conservative	0; Mismatches 0; Indels 0; Gaps
Db	133 greek:khadapayfipss 153	
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PF 07-AMV-1993; 111208.
PA (HISD)-1993; DP-111208.
PA (KUNS ) KUNIMAF CO LTD.
DA WPI; 95-04020/06/.
DR TRENDS; Q79939.
PT Tobacco plants producing anti-tobacco mosaic virus
PT monoclonal antibody-producing animal-derived anti-virus antibody -
Example 2; pages 13-14, 28pp; Japanese.
CC chain cod at 2530, encode 166757 and 166758, the light and heavy
CC monoclonal antibody. The chain was tobacco mosaic virus (TMV)
CC plasmid vector, which was incorporated into A. tumefaciens.
CC tobacco plant expression vector was used to transform
CC also be derived from TMV resistant, the plants could
Sequence 219 AA;
Query Match: Beat Local Similarity 100.0% Score 22 DB 13; Length 219;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps
DB 136 gtttctatgactgttcattggaa 147
OY 121 GTTCTATGACTGTTCATTGGAA 142

RESULT 44
ID R39573; standard: Protein: 667 AA.
AC R39573;
CD Single chain Fv polypeptide; VH-VL heterodimer; Immunoglobulin Ig;
DE Single chain Fv polypeptide; VH-VL heterodimer; Immunoglobulin Ig;
EV protoxin.
FZ Peptidomimetic
PD 19-AUG-1993.
PF 05-FEB-1993; 001055.
PF 06-FEB-1993; US 631967.
PR (CHEN-) CRYSTALLOGRAPHIC CORP.
PA (CHEN-) CRYSTALLOGRAPHIC CORP.
PI Houston TX, Bantec 35 Oppermann H, Ring DB;
DR WPI; 95-27288/34.
PT New monoclonal antibody for lysating or treating breast or ovarian cancer etc.
PT antigen - for lysating or treating breast or ovarian cancer etc.
PC Example; pages 71-74; 87pp; English.
C1 tumor 2; refers to a protein antigen expressed on the surface of
approx. 200,000 mol. wt. acidic glycoprotein having an isotactic

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[illegible]

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CC      is a conserved 5.3' [see Q4808], R39568). A single chain PV (spV)
CC      is a gene fusion product of the SV40 retroviral vector and the
CC      a gene fusion including viral and cellular sequences. The protein
CC      a peptide-encoding linker. Such linker sequences are part of the 16 kDa
CC      MA residue 181-135 in G39559; which includes some of the 16 kDa
CC      antibody sequence in R1957. Using Q46084 for the 320CV monoclonal
CC      binding affinity for a c-erbB receptor can be produced having a
CC      the pseudotonal, extron fragment analogous to cysteine A other design
CC      is fused to the carboxy terminus of the antic-c-erbB-2 741 sry
CC      protein, which was reported as a single-chain PV-toxin fusion
CC      which initially was left on the protein. It remains short PD leader
CC      Sequence 667 MA:
DB       Query Match          13.7% Score 32 DB 3 Length 667:
DB       Best Local Similarity 100.0% Pval 0.95E-17:
DB       Matches 23 Conservative 0 Mismatches 0 Indels 0 Gaps 0
DB       236 gxi1xixadnaparipps 257
DB       |||||
DB       121 CTTLETNDDAPFPIPSPPS 142
DB       |||||
DB       RESULT 45
ID       RI5440 1992 (first entry) 125 AA.
ID       RI5440 1992 (last entry) 125 AA.
DE       Lymphoblastic leukemia cell line derived from NB 2C2.
DE       Lymphoblastic leukemia cell line derived from NB 2C2.
FM       HMYT, TGM-1; antigen-binding fragments; inflammation;
FM       auto-immune disease.
PM       Howo antigens.
PM       Howo antigens.
PD       04-DEC-1991.
PD       01-JUN-1990 US-532001.
PD       25-MAY-1991; 201243.
PR       COLORED KERNER & CO INC.
PR       COLORED KERNER & CO INC.
PT       WPI: 91-35585G/43.
PT       Microbially-expressed portions of monoclonal antibodies can block
PT       attachment of rhinovirus ligands to inter-cellular adhesion
P5       Chain 1: Page 20 289P English
P5       Chain 1: Page 20 289P English
CC       This is one of six antibody fragments from MBH's specific for desmin
CC       1 of TGM-1. The antibody fragments can be used to treat or prevent
CC       monovirus infection. See RI5437-RI5443.
CC       Sequence 125 AA.
Query Match          14.5% Score 21 DB 3 Length 125:
DB       Best Local Similarity 100.0% Pval 1.73E-15:
```


971 5 3.4 1462 1 TM6 CAEL 1462 1 1.45e+03
 972 5 3.4 1464 1 TM6 CAEL 1464 1 1.45e+03
 973 5 3.4 1466 1 TM6 CAEL 1466 1 1.45e+03
 974 5 3.4 1468 1 TM6 CAEL 1468 1 1.45e+03
 975 5 3.4 1470 1 TM6 CAEL 1470 1 1.45e+03
 976 5 3.4 1472 1 TM6 CAEL 1472 1 1.45e+03
 977 5 3.4 1474 1 TM6 CAEL 1474 1 1.45e+03
 978 5 3.4 1476 1 TM6 CAEL 1476 1 1.45e+03
 979 5 3.4 1478 1 TM6 CAEL 1478 1 1.45e+03
 980 5 3.4 1480 1 TM6 CAEL 1480 1 1.45e+03
 981 5 3.4 1482 1 TM6 CAEL 1482 1 1.45e+03
 982 5 3.4 1484 1 TM6 CAEL 1484 1 1.45e+03
 983 5 3.4 1486 1 TM6 CAEL 1486 1 1.45e+03
 984 5 3.4 1488 1 TM6 CAEL 1488 1 1.45e+03
 985 5 3.4 1490 1 TM6 CAEL 1490 1 1.45e+03
 986 5 3.4 1492 1 TM6 CAEL 1492 1 1.45e+03
 987 5 3.4 1494 1 TM6 CAEL 1494 1 1.45e+03
 988 5 3.4 1496 1 TM6 CAEL 1496 1 1.45e+03
 989 5 3.4 1498 1 TM6 CAEL 1498 1 1.45e+03
 990 5 3.4 1500 1 TM6 CAEL 1500 1 1.45e+03
 991 5 3.4 1502 1 TM6 CAEL 1502 1 1.45e+03
 992 5 3.4 1504 1 TM6 CAEL 1504 1 1.45e+03
 993 5 3.4 1506 1 TM6 CAEL 1506 1 1.45e+03
 994 5 3.4 1508 1 TM6 CAEL 1508 1 1.45e+03
 995 5 3.4 1510 1 TM6 CAEL 1510 1 1.45e+03
 996 5 3.4 1512 1 TM6 CAEL 1512 1 1.45e+03
 997 5 3.4 1514 1 TM6 CAEL 1514 1 1.45e+03
 998 5 3.4 1516 1 TM6 CAEL 1516 1 1.45e+03
 999 5 3.4 1518 1 TM6 CAEL 1518 1 1.45e+03
 1000 5 3.4 1520 1 TM6 CAEL 1520 1 1.45e+03

ALIGNMENTS

RESULT 1
 ID KRCJMOUSE STANDARD: PRT: 130 AA.
 AC P01607: 130 AA.
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DE IC KAPPA CHAIN PRECURSOR V-V REGION (MOPC 41).
 OC EUTHERIA, RODENTIA.
 RN (1)
 RA MEDLINE: 8109866.
 RL NATURE 280:370-375(1979).
 RP SEQUENCE OF 1-33.

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CELL 21:793-799(1980).
 DR EMBL: R00880: C197444.
 DR PIR: A01924: KWSJB.
 RN IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 22
 FT CHAIN 23 117
 FT DOMAIN 23 45
 FT FRAMEWORK 1 45
 FT COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 23 45
 FT FRAMEWORK 2 45
 FT COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 23 45
 FT FRAMEWORK 3 45
 FT COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 45 110
 FT NON_TER 117
 FT SEQUENCE 117 AA: 12954 MW: 3872806 CMC32.

Query Match 11.4% Score 18; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2,646-21; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 21 NCBI/NTS/SSLSISG 38
 QY 19 NCBI/NTS/SSLSISG 36

RESULT 3
 ID KRCJMOUSE STANDARD: PRT: 117 AA.
 AC P01607: 117 AA.
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DE IC KAPPA CHAIN PRECURSOR V-V REGION (MOPC 41).
 OC EUTHERIA, RODENTIA.
 RN (1)
 RA MEDLINE: 8109866.
 RL NATURE 280:370-375(1979).
 RP SEQUENCE FROM N.A.
 RX BEUTLEY D.L., BABBITTS T.H.:
 DR EMBL: K01324: C18598.
 DR EMBL: K01324: C18598.
 DR EMBL: K01324: C18598.
 DR EMBL: K01324: C18598.
 DR PIR: A01881: KIRH01.

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EX MEDLINE: 77148216.
 RA BEUTLEY D.L., BABBITTS T.H.:
 RN (1)
 RA BEUTLEY D.L., BABBITTS T.H.:
 DR EMBL: K01324: C18598.
 DR EMBL: K01324: C18598.
 DR EMBL: K01324: C18598.
 DR EMBL: K01324: C18598.
 DR PIR: A01881: KIRH01.
 DR HSP: P01607: 695A.
 RN IMMUNOGLOBULIN V REGION: SIGNAL; BENCE-JONES PROTEIN.
 FT SIGNAL 1 22
 FT CHAIN 23 117
 FT DOMAIN 23 45
 FT FRAMEWORK 1 45
 FT COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 23 45
 FT FRAMEWORK 2 45
 FT COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 23 45
 FT FRAMEWORK 3 45
 FT COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 45 110
 FT NON_TER 117
 FT SEQUENCE 117 AA: 12954 MW: 3872806 CMC32.

Query Match 20.8% Score 29; DB 1; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2,646-21; Indels 0; Gaps 0;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 76 SVR/NTS/SSLSISG 106
 QY 76 SVR/NTS/SSLSISG 106

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PIR: A21056: A21056.
 DR HSP: P01607: 1079.
 RN IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 22
 FT CHAIN 23 117
 FT DOMAIN 23 45
 FT FRAMEWORK 1 45
 FT COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 23 45
 FT FRAMEWORK 2 45
 FT COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 23 45
 FT FRAMEWORK 3 45
 FT COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 45 110
 FT NON_TER 117
 FT SEQUENCE 117 AA: 12799 MW: 3020361 CMC32.

Query Match 11.0% Score 16; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2,646-21; Indels 0; Gaps 0;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 21 NCBI/NTS/SSLSISG 36
 QY 19 NCBI/NTS/SSLSISG 34

RESULT 4
 ID KRCJMOUSE STANDARD: PRT: 129 AA.
 AC P04631: 129 AA.
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-OCT-1993 (REL. 27, LAST SEQUENCE UPDATE)
 DE IC KAPPA CHAIN PRECURSOR V-V REGION (MOPC 41).
 OC EUTHERIA, RODENTIA.
 RN (1)
 RA MEDLINE: 8501416.
 RL NATURE 280:370-375(1979).
 RP SEQUENCE FROM N.A.
 RX BEUTLEY D.L., BABBITTS T.H.:
 DR EMBL: K01324: C18598.
 DR EMBL: K01324: C18598.
 DR EMBL: K01324: C18598.
 DR EMBL: K01324: C18598.
 DR PIR: A01881: KIRH01.
 DR HSP: P01607: 370A.
 RN IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 22
 FT CHAIN 23 129
 FT DOMAIN 23 45
 FT FRAMEWORK 1 45
 FT COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 23 45
 FT FRAMEWORK 2 45
 FT COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 23 45
 FT FRAMEWORK 3 45
 FT COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 45 110
 FT NON_TER 119
 FT SEQUENCE 129 AA: 12799 MW: 3020361 CMC32.

DR HSP: A01874; K1HRY.
 DR HSP: P01607; 11GM.
 KW IMMUNOGLOBULIN V REGION: BENICE-JONES PROTEIN.
 FT DOMAIN 1 23 FRAMENOR 1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 45 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 5 67 FRAMENOR 3.
 FT DOMAIN 6 78 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 7 89 BY SIMILARITY.
 FT DISULFID 108 108
 FT NON-TER 108 108
 SO SEQUENCE 108 AA: 11782 MW: 98776875 CRC32:
 Query Match
 Best Local Similarity 100.0%
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 14
 ID FVIR.HUMAN STANDARD: PRT: 108 AA.
 AC P01610: 1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN V-I REGION (HAT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUKARYOTA: PRIMATES.
 CC - THIS CHAIN WAS ISOLATED FROM A PATIENT WITH
 3,4-PYRIDYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 WADENSTROM'S MACROGLOBULINEMIA.
 DR PIR: A01874; K1HRY.
 KW IMMUNOGLOBULIN V REGION: MONOCLONAL ANTIBODY.
 FT DOMAIN 1 23 FRAMENOR 1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 45 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 4 56 FRAMENOR 3.
 FT DOMAIN 5 67 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 6 78 BY SIMILARITY.
 FT DISULFID 98 107
 FT NON-TER 98 107
 SO SEQUENCE 108 AA: 11809 MW: 4539462 CRC32:
 Query Match
 Best Local Similarity 100.0%
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 16
 ID FVIR.HUMAN STANDARD: PRT: 108 AA.
 AC P01612: 1985 (REL. 32, CREATED)
 DT 01-JAN-1988 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN V-I REGION (HAT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUKARYOTA: PRIMATES.
 CC - THIS IS A BENICE-JONES PROTEIN.
 DR PIR: A01867; 11VC.
 KW IMMUNOGLOBULIN V REGION: BENICE-JONES PROTEIN.
 FT DOMAIN 1 23 FRAMENOR 1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 45 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 5 67 FRAMENOR 3.
 FT DOMAIN 6 78 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 108 108
 FT NON-TER 108 108
 SO SEQUENCE 108 AA: 11737 MW: 4142386 CRC32:
 Query Match
 Best Local Similarity 100.0%
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 17
 ID FVIR.HUMAN STANDARD: PRT: 108 AA.
 AC P01600: 1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN V-I REGION (HAT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUKARYOTA: PRIMATES.
 CC - THIS CHAIN WAS ISOLATED FROM A PATIENT WITH
 3,4-PYRIDYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 WADENSTROM'S MACROGLOBULINEMIA.
 DR PIR: A01874; K1HRY.
 KW IMMUNOGLOBULIN V REGION: MONOCLONAL ANTIBODY.
 FT DOMAIN 1 23 FRAMENOR 1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 45 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 4 56 FRAMENOR 3.
 FT DOMAIN 5 67 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 6 78 BY SIMILARITY.
 FT DISULFID 98 107
 FT NON-TER 98 107
 SO SEQUENCE 108 AA: 11809 MW: 4539462 CRC32:
 Query Match
 Best Local Similarity 100.0%
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PT DISULFID 73 88 BY SIMILARITY.
 FT NON-TER 108 108
 SO SEQUENCE 108 AA: 11840 MW: 884251 CRC32:
 Query Match
 Best Local Similarity 100.0%
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
 ID FVIR.HUMAN STANDARD: PRT: 108 AA.
 AC P01615: 1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 37, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN V-I REGION (HAT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUKARYOTA: PRIMATES.
 CC - THIS CHAIN WAS ISOLATED FROM A PATIENT WITH
 3,4-PYRIDYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 WADENSTROM'S MACROGLOBULINEMIA.
 DR PIR: A01874; K1HRY.
 KW IMMUNOGLOBULIN V REGION: MONOCLONAL ANTIBODY.
 FT DOMAIN 1 23 FRAMENOR 1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 45 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 4 56 FRAMENOR 3.
 FT DOMAIN 5 67 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 6 78 BY SIMILARITY.
 FT DISULFID 108 108
 FT NON-TER 108 108
 SO SEQUENCE 108 AA: 11809 MW: 4539462 CRC32:
 Query Match
 Best Local Similarity 100.0%
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN V-I REGION (HAT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUKARYOTA: PRIMATES.
 CC - THIS IS A BENICE-JONES PROTEIN.
 DR PIR: A01867; 11VC.
 KW IMMUNOGLOBULIN V REGION: BENICE-JONES PROTEIN.
 FT DOMAIN 1 23 FRAMENOR 1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 45 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 4 56 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 5 67 FRAMENOR 3.
 FT DOMAIN 6 78 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 108 108
 FT NON-TER 108 108
 SO SEQUENCE 108 AA: 11671 MW: 4142386 CRC32:
 Query Match
 Best Local Similarity 100.0%
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 18
 ID FVIR.HUMAN STANDARD: PRT: 108 AA.
 AC P01615: 1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN V-I REGION (HAT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUKARYOTA: PRIMATES.
 CC - THIS CHAIN WAS ISOLATED FROM A PATIENT WITH
 3,4-PYRIDYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
 WADENSTROM'S MACROGLOBULINEMIA.
 DR PIR: A01874; K1HRY.
 KW IMMUNOGLOBULIN V REGION: MONOCLONAL ANTIBODY.
 FT DOMAIN 1 23 FRAMENOR 1.
 FT DOMAIN 2 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 45 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 4 56 FRAMENOR 3.
 FT DOMAIN 5 67 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 6 78 BY SIMILARITY.
 FT DISULFID 108 108
 FT NON-TER 108 108
 SO SEQUENCE 108 AA: 11809 MW: 4539462 CRC32:
 Query Match
 Best Local Similarity 100.0%
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RE BLOCHIN 2 133.945-950(1971).
 CC -1- THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 DR PIR: A01855; KIRDE.
 DB HSP: P01607; 1PVC.
 RE IMMUNOGLOBULIN V REGION.
 FT DOMAIN 2 24 33 FRAMESWORK 1
 FT DOMAIN 3 35 49 FRAMESWORK 2
 FT DOMAIN 4 50 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 5 57 88 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 6 58 88 FRAMESWORK 3
 FT DOMAIN 7 98 107 FRAMESWORK 4
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON-TER 108 108
 SQ SEQUENCE 108 AA: 11661 MW: 10844493 CMC32.
 Query Match 9.7%: Score 14; DB 1; Length 108;
 Best Local Similarity 85.7%: Pred. No. 3,54e-16;
 Matches 14: Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 1 BICHOCHER 14
 QY 21 DICTYOSPSSISAS 34

RESULT 19
 ID KY15 MOUSE STANDARD: PRT: 108 AA.
 AC P01610
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-REGION (J606).
 OC EUTHERIA: RODENTIA.
 CC -1- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND
 PIR: A01811; KIRDE.
 DR HSP: P01607; 1PVC.
 RE IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23 23 FRAMESWORK 1
 FT DOMAIN 2 24 49 FRAMESWORK 2
 FT DOMAIN 3 50 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 4 57 88 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 89 97 FRAMESWORK 3
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON-TER 108 108
 SQ SEQUENCE 108 AA: 10844493 CMC32.
 Query Match 9.7%: Score 14; DB 1; Length 108;
 Best Local Similarity 85.7%: Pred. No. 3,54e-16;
 Matches 14: Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Db 1 BICHOCHER 14
 QY 21 DICTYOSPSSISAS 34

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FT NON-TER 108 108
 SQ SEQUENCE 108 AA: 8455AF00 CMC32.
 Query Match 9.7%: Score 14; DB 1; Length 108;
 Best Local Similarity 100.0%: Pred. No. 3,54e-16;
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 DICTYOSPSSISAS 34
 QY 21 DICTYOSPSSISAS 34

RESULT 21
 ID KY15 MOUSE STANDARD: PRT: 113 AA.
 AC P01610
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-REGION (J606).
 OC EUTHERIA: RODENTIA.
 CC -1- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND
 PIR: A01811; KIRDE.
 DR HSP: P01607; 1PVC.
 RE IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 24 33 FRAMESWORK 1
 FT DOMAIN 2 34 49 FRAMESWORK 2
 FT DOMAIN 3 50 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 4 57 88 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 89 97 FRAMESWORK 3
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON-TER 113 113
 SQ SEQUENCE 113 AA: 12496 MW: A067008 CMC32.
 Query Match 9.7%: Score 14; DB 1; Length 113;
 Best Local Similarity 100.0%: Pred. No. 3,54e-16;
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 100 PYTGCGTLEIKR 113
 QY 115 PYTGCGTLEIKR 128

RESULT 23
 ID KY15 MOUSE STANDARD: PRT: 106 AA.
 AC P01835
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-REGION (J606).
 OC EUTHERIA: RODENTIA.
 CC -1- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND
 PIR: A01811; KIRDE.
 DR HSP: P01607; 1PVC.
 RE IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 24 33 FRAMESWORK 1
 FT DOMAIN 2 34 49 FRAMESWORK 2
 FT DOMAIN 3 50 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 4 57 88 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 89 97 FRAMESWORK 3
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON-TER 106 106
 SQ SEQUENCE 106 AA: 8455AF00 CMC32.
 Query Match 9.7%: Score 14; DB 1; Length 106;
 Best Local Similarity 100.0%: Pred. No. 3,54e-16;
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 100 PYTGCGTLEIKR 113
 QY 115 PYTGCGTLEIKR 128

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FT DOMAIN 98 108 FRAMESWORK 4
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON-TER 108 108
 SQ SEQUENCE 108 AA: 11810 MW: 8598947 CMC32.
 Query Match 9.7%: Score 14; DB 1; Length 108;
 Best Local Similarity 100.0%: Pred. No. 3,54e-16;
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 95 PYTGCGTLEIKR 108
 QY 115 PYTGCGTLEIKR 128

RESULT 20
 ID KY15 MOUSE STANDARD: PRT: 108 AA.
 AC P01835
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-REGION (J606).
 OC EUTHERIA: RODENTIA.
 CC -1- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND
 PIR: A01811; KIRDE.
 DR HSP: P01607; 1PVC.
 RE IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23 23 FRAMESWORK 1
 FT DOMAIN 2 24 49 FRAMESWORK 2
 FT DOMAIN 3 50 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 4 57 88 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 89 97 FRAMESWORK 3
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON-TER 108 108
 SQ SEQUENCE 108 AA: 8455AF00 CMC32.
 Query Match 9.7%: Score 14; DB 1; Length 108;
 Best Local Similarity 100.0%: Pred. No. 3,54e-16;
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 100 PYTGCGTLEIKR 113
 QY 115 PYTGCGTLEIKR 128

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RESULT 22
 ID KY15 MOUSE STANDARD: PRT: 113 AA.
 AC P01835
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-REGION (J606).
 OC EUTHERIA: RODENTIA.
 CC -1- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND
 PIR: A01811; KIRDE.
 DR HSP: P01607; 1PVC.
 RE IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 24 33 FRAMESWORK 1
 FT DOMAIN 2 34 49 FRAMESWORK 2
 FT DOMAIN 3 50 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 4 57 88 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 89 97 FRAMESWORK 3
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON-TER 113 113
 SQ SEQUENCE 113 AA: 11390 MW: 644552AE CMC32.
 Query Match 9.7%: Score 14; DB 1; Length 113;
 Best Local Similarity 100.0%: Pred. No. 3,54e-16;
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 100 PYTGCGTLEIKR 113
 QY 115 PYTGCGTLEIKR 128

RESULT 23
 ID KY15 MOUSE STANDARD: PRT: 106 AA.
 AC P01835
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1993 (REL. 27, LAST ANNOTATION UPDATE)
 DE IG KAPPA CHAIN V-REGION (J606).
 OC EUTHERIA: RODENTIA.
 CC -1- THIS CHAIN WAS ISOLATED FROM MYELOMA PROTEINS THAT BIND
 PIR: A01811; KIRDE.
 DR HSP: P01607; 1PVC.
 RE IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 24 33 FRAMESWORK 1
 FT DOMAIN 2 34 49 FRAMESWORK 2
 FT DOMAIN 3 50 56 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 4 57 88 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 89 97 FRAMESWORK 3
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON-TER 106 106
 SQ SEQUENCE 106 AA: 8455AF00 CMC32.
 Query Match 9.7%: Score 14; DB 1; Length 106;
 Best Local Similarity 100.0%: Pred. No. 3,54e-16;
 Matches 14: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 100 PYTGCGTLEIKR 113
 QY 115 PYTGCGTLEIKR 128

OC EUMARTON, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA;
 OC EUTHERIA, RODENTIA.
 RN [1]
 RP SEQUENCE: 79073152
 RA WEIGER W., GATTAHAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 CC -1- THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.
 DR PIR: A01930; RMS80.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23 FRAMWORK 1.
 FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 54 FRAMWORK 2.
 FT DOMAIN 4 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 92 FRAMWORK 3.
 FT DOMAIN 6 93 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 7 101 FRAMWORK 4.
 FT DISULFID 102 111 BY SIMILARITY.
 FT NON_TER 111 111
 FT SEQUENCE 111 AA: 11980 MW: APC944E CRC32:
 SO SEQUENCE 111 AA: 11980 MW: APC944E CRC32:
 Query Match 7.64; Score 11: DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6,366-09;
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 101 TPGCCTLEIK 111
 QY 117 TPGCCTLEIK 127

RESULT 49
 ID EVAL MOOSE STANDARD: PRT: 111 AA.
 AC P01672.
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1989 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN V-III REGION (MOG 78).
 OS MUS MUSCULUS (MOUSE).
 OC EUMARTON, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA;
 OC EUTHERIA, RODENTIA.
 RN [1]
 RP SEQUENCE: 67056897.
 RA GRAY W.R., BREYER W.J., HOOD L.E.;
 RL SCIENCE 155:485-487(1987).
 CC -1- THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.
 DR PIR: A01930; RMS80.
 KW IMMUNOGLOBULIN V REGION; BENKE-JONES PROTEIN.
 FT DOMAIN 1 23 FRAMWORK 1.
 FT SEQUENCE 111 AA: 11980 MW: APC944E CRC32:
 SO SEQUENCE 111 AA: 11980 MW: APC944E CRC32:

DB 101 TPGCCTLEIK 111
 QY 117 TPGCCTLEIK 127
 Search completed: Thu Apr 15 18:03:29 1999
 Job time : 52 secs.

FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 54 FRAMWORK 2.
 FT DOMAIN 4 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 92 FRAMWORK 3.
 FT DOMAIN 6 93 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 102 111 BY SIMILARITY.
 FT NON_TER 111 111
 FT SEQUENCE 111 AA: 11980 MW: APC944E CRC32:
 SO SEQUENCE 111 AA: 11980 MW: APC944E CRC32:
 Query Match 7.64; Score 11: DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6,366-09;
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 101 TPGCCTLEIK 111
 QY 117 TPGCCTLEIK 127

RESULT 50
 ID EVAL MOOSE STANDARD: PRT: 111 AA.
 AC P01672.
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1989 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG KAPPA CHAIN V-III REGION (PC 7940).
 OS MUS MUSCULUS (MOUSE).
 OC EUMARTON, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA;
 OC EUTHERIA, RODENTIA.
 RN [1]
 RP SEQUENCE: 79073152.
 RA WEIGER W., GATTAHAN L., LOH E., SCHILLING J., HOOD L.E.;
 RL NATURE 276:785-790(1978).
 CC -1- THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.
 DR PIR: C01938; RMS80.
 KW IMMUNOGLOBULIN V REGION.
 FT DOMAIN 1 23 FRAMWORK 1.
 FT DOMAIN 2 38 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 3 54 FRAMWORK 2.
 FT DOMAIN 4 61 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 5 92 FRAMWORK 3.
 FT DOMAIN 6 93 COMPLEMENTARITY-DETERMINING 3.
 FT DISULFID 102 111 BY SIMILARITY.
 FT NON_TER 111 111
 FT SEQUENCE 111 AA: 11980 MW: APC944E CRC32:
 SO SEQUENCE 111 AA: 11980 MW: APC944E CRC32:

Query Match 7.64; Score 11: DB 1; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6,366-09;
 Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

!!SEQUENCE LIST 1.0
(Peptide) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-2 check: 4259 from: 1

FROMIG of: /home/obryen/ree455/olig/US08836455.pep
sequence 2, application us/08836455

general information:
applicant: chatterjee, malaya
applicant: loon, kenneth a.
applicant: chatterjee, sunil k. . .

TO: swp: * Sequences: 254,782 Total-length: 82,009,484 April 18, 1999 20:25

Database Release Information:

2 databases: SWISS-PROT, Release 36.0, Released on 18Jul1998, Formatted on 18Aug1998
Combined 2 SPTREMBL, Release 8.0, Released on 21Nov1998, Formatted on 15Dec1998

Word-size: 5 Words: 77835 Diagonals: 14,908 Total-diagonals: 118,698,092
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 9.51

Sequence Stnd Diag Score Width Documentation ..

SM:KV5G_MOUSE	+	2	116	1	P01639	mus musculus (mouse).	1g kappe
SM:KV5H_MOUSE	+	2	70	1	P01641	mus musculus (mouse).	1g kappe
SM:KV5O_MOUSE	+	-20	46	1	P01648	mus musculus (mouse).	1g kappe
SM:KV5M_MOUSE	+	-20	46	1	P01646	mus musculus (mouse).	1g kappe
SM:KV5N_MOUSE	+	-20	45	1	P01647	mus musculus (mouse).	1g kappe
SM:KV5L_MOUSE	+	-20	45	1	P01645	mus musculus (mouse).	1g kappe
SM:KV5K_MOUSE	+	-20	45	1	P01644	mus musculus (mouse).	1g kappe
SM:KV5U_MOUSE	+	-20	40	1	P04946	mus musculus (mouse).	1g kappe
SM:KV1Y_HUMAN	+	-20	39	1	P80362	homo sapiens (human).	1g kappe
SM:KV5T_MOUSE	+	-20	38	1	P01653	mus musculus (mouse).	1g kappe
SM:KV5S_MOUSE	+	-20	38	1	P01652	mus musculus (mouse).	1g kappe
SM:KV5Q_MOUSE	+	-20	38	1	P01650	mus musculus (mouse).	1g kappe
SM:KV5P_MOUSE	+	-20	38	1	P01649	mus musculus (mouse).	1g kappe
SM:KV5J_MOUSE	+	-20	38	1	P01643	mus musculus (mouse).	1g kappe
SM:KV1R_HUMAN	+	-20	36	1	P01610	homo sapiens (human).	1g kappe
SM:KV5E_MOUSE	+	-20	36	1	P01637	mus musculus (mouse).	1g kappe
SM:KV1S_HUMAN	+	-20	35	1	P01611	homo sapiens (human).	1g kappe
SM:KV1G_HUMAN	+	-20	35	1	P01599	homo sapiens (human).	1g kappe
SM:KV1X_HUMAN	+	-20	34	1	P04432	homo sapiens (human).	1g kappe
SM:KV1O_HUMAN	+	-20	34	1	P01607	homo sapiens (human).	1g kappe
SM:KV5F_MOUSE	+	0	33	1	P01638	mus musculus (mouse).	1g kappe
SM:KV1A_HUMAN	+	-20	32	1	P01593	homo sapiens (human).	1g kappe
SM:KV1P_HUMAN	+	-20	31	1	P01608	homo sapiens (human).	1g kappe
SM:KV1H_HUMAN	+	-20	31	1	P01600	homo sapiens (human).	1g kappe
SM:KV5R_MOUSE	+	-20	29	1	P01651	mus musculus (mouse).	1g kappe
SM:KV1N_HUMAN	+	-20	28	1	P01606	homo sapiens (human).	1g kappe
SM:KV1V_HUMAN	+	-20	27	1	P04430	homo sapiens (human).	1g kappe
SM:KV1J_HUMAN	+	2	27	1	P01602	homo sapiens (human).	1g kappe
SM:KV1C_HUMAN	+	2	27	1	P01601	homo sapiens (human).	1g kappe
SM:KV1D_HUMAN	+	-20	27	1	P01595	homo sapiens (human).	1g kappe
SM:KV5D_MOUSE	+	-20	26	1	P01596	homo sapiens (human).	1g kappe
SM:KV1L_HUMAN	+	-20	26	1	P01636	mus musculus (mouse).	1g kappe
SM:KV5C_MOUSE	+	-20	25	1	P01604	homo sapiens (human).	1g kappe
SM:KV5Q_MOUSE	+	0	25	1	P01635	mus musculus (mouse).	1g kappe
SM:KV1T_HUMAN	+	-20	24	2	P01612	homo sapiens (human).	1g kappe
SM:KV1Q_HUMAN	+	-20	24	1	P01609	homo sapiens (human).	1g kappe
SM:KV1B_HUMAN	+	-20	24	1	P01594	homo sapiens (human).	1g kappe
SM:KV6A_MOUSE	+	-21	24	2	P01675	mus musculus (mouse).	1g kappe
SM:KV3K_HUMAN	+	0	24	2	P06311	homo sapiens (human).	1g kappe
SM:KV6D_MOUSE	+	-21	24	2	P01678	mus musculus (mouse).	1g kappe
SM:KV3D_MOUSE	+	-16	23	1	P03977	mus musculus (mouse).	1g kappe
SM:KV5B_MOUSE	+	9	23	1	P01634	mus musculus (mouse).	1g kappe
SP:RO:P80913	+	3	23	2	P80913	mus musculus (mouse).	1g kappe
SM:KV1X_HUMAN	+	-20	22	1	P01605	homo sapiens (human).	1g kappe
SM:KV3C_MOUSE	+	-16	21	1	P01656	mus musculus (mouse).	1g kappe
SM:KV3A_MOUSE	+	-16	21	1	P01654	mus musculus (mouse).	1g kappe
SM:KV1F_HUMAN	+	-20	21	1	P01598	homo sapiens (human).	1g kappe
SM:KV1E_HUMAN	+	-20	21	1	P01597	homo sapiens (human).	1g kappe
SP_HUM:O15533	+	-17	21	1	O15533	homo sapiens (human).	dna real

of seqs identified at least 5 aa long

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RESULT 1
ID 013538 PRELIMINARY: PRT: 117 M.
AC 013538
DT 01-JAN-1998 (TREMBLIER, 05, CREATED)
DT 01-JAN-1998 (TREMBLIER, 07, LAST SEQUENCE UPDATE)
DE 1-NOV-1996 (TREMBLIER, 01, LAST ANNOTATION UPDATE)
OC ETHYRIA, PRIMATES
GN VIA SAPIENS (HUMAN)
RA SHARON F., DOAN L., END N., BLAGERA O., POWERANTE R.J.
RM MEDLINE 9621146
RL EMBL 148716: G2289026
DR EMBL 148716: G2289026
SQ SEQUENCE 262 AA: 27842 MW: 4724086 CMC32;
KX RNA-DIRECTED DNA POLYMERASE
KW RNA-DIRECTED DNA POLYMERASE
NC

ALIGNMENTS

DAGSHUND VARIANT 2. 3.16e+03
DAGSHUND VARIANT 1. 3.16e+03
P-TYPE ATPASE 2. 3.16e+03
LATS. ANTICEN. CYPOLAS 3.16e+03
PUDATIVE METL-CAN. STIR 3.16e+03
CHITIN SYNTHASE 3.16e+03
NEUROSPICIN (FRAGMENT) 3.16e+03
FILAGGRIN (FRAGMENT) 3.16e+03
KIM187 PROTEIN 3.16e+03
CHROMOSOME XY READING 3.16e+03
HYPOHETICAL 151.9 KD 3.16e+03
PRENATAL STORAGE CLIC 3.16e+03
P7B12.4. 3.16e+03
90K-PROTEASE (BACILLUS) 3.16e+03
NUCLEAR RECEPTOR COACT 3.16e+03
COSMID Y7.1. ASPARAGINE R 3.16e+03
B18A. PROTEIN. 3.16e+03
COCTEST WALL PROTEIN PR 3.16e+03
PROPHOSPHOLIPID 2. -IN 3.16e+03
DSE2. 3.16e+03
EMERSONIC MUSCLE MYOSIN 3.16e+03
ALPHA-CARDIAC MYOSIN H 3.16e+03
COILED COIL RT C. ELKMAN 3.16e+03
NUCLEAR PORE 3.16e+03
VOLUME-DEPENDENT L-TY 3.16e+03
REMOVAL CALCIUM CHAIN 3.16e+03
LCAN PROTEIN. 3.16e+03
RANODINE RECEPTOR HOM 3.16e+03

RESULT 1
ID 013538 PRELIMINARY: PRT: 117 M.
AC 013538
DT 01-JAN-1998 (TREMBLIER, 05, CREATED)
DT 01-JAN-1998 (TREMBLIER, 07, LAST SEQUENCE UPDATE)
DE 1-NOV-1996 (TREMBLIER, 01, LAST ANNOTATION UPDATE)
OC ETHYRIA, PRIMATES
GN VIA SAPIENS (HUMAN)
RA SHARON F., DOAN L., END N., BLAGERA O., POWERANTE R.J.
RM MEDLINE 9621146
RL EMBL 148716: G2289026
DR EMBL 148716: G2289026
SQ SEQUENCE 262 AA: 27842 MW: 4724086 CMC32;
KX RNA-DIRECTED DNA POLYMERASE
KW RNA-DIRECTED DNA POLYMERASE
NC

ALIGNMENTS

DAGSHUND VARIANT 2. 3.16e+03
DAGSHUND VARIANT 1. 3.16e+03
P-TYPE ATPASE 2. 3.16e+03
LATS. ANTICEN. CYPOLAS 3.16e+03
PUDATIVE METL-CAN. STIR 3.16e+03
CHITIN SYNTHASE 3.16e+03
NEUROSPICIN (FRAGMENT) 3.16e+03
FILAGGRIN (FRAGMENT) 3.16e+03
KIM187 PROTEIN 3.16e+03
CHROMOSOME XY READING 3.16e+03
HYPOHETICAL 151.9 KD 3.16e+03
PRENATAL STORAGE CLIC 3.16e+03
P7B12.4. 3.16e+03
90K-PROTEASE (BACILLUS) 3.16e+03
NUCLEAR RECEPTOR COACT 3.16e+03
COSMID Y7.1. ASPARAGINE R 3.16e+03
B18A. PROTEIN. 3.16e+03
COCTEST WALL PROTEIN PR 3.16e+03
PROPHOSPHOLIPID 2. -IN 3.16e+03
DSE2. 3.16e+03
EMERSONIC MUSCLE MYOSIN 3.16e+03
ALPHA-CARDIAC MYOSIN H 3.16e+03
COILED COIL RT C. ELKMAN 3.16e+03
NUCLEAR PORE 3.16e+03
VOLUME-DEPENDENT L-TY 3.16e+03
REMOVAL CALCIUM CHAIN 3.16e+03
LCAN PROTEIN. 3.16e+03
RANODINE RECEPTOR HOM 3.16e+03

RESULT 2
ID 013542 PRELIMINARY: PRT: 262 M.
AC 013542
DT 01-JAN-1998 (TREMBLIER, 05, CREATED)
DT 01-JAN-1998 (TREMBLIER, 07, LAST SEQUENCE UPDATE)
DE 1-NOV-1996 (TREMBLIER, 01, LAST ANNOTATION UPDATE)
OC ETHYRIA, PRIMATES
GN VIA SAPIENS (HUMAN)
RA SHARON F., DOAN L., END N., BLAGERA O., POWERANTE R.J.
RM MEDLINE 9621146
RL EMBL 148716: G2289026
DR EMBL 148716: G2289026
SQ SEQUENCE 262 AA: 27842 MW: 4724086 CMC32;
KX RNA-DIRECTED DNA POLYMERASE
KW RNA-DIRECTED DNA POLYMERASE
NC

ALIGNMENTS

DAGSHUND VARIANT 2. 3.16e+03
DAGSHUND VARIANT 1. 3.16e+03
P-TYPE ATPASE 2. 3.16e+03
LATS. ANTICEN. CYPOLAS 3.16e+03
PUDATIVE METL-CAN. STIR 3.16e+03
CHITIN SYNTHASE 3.16e+03
NEUROSPICIN (FRAGMENT) 3.16e+03
FILAGGRIN (FRAGMENT) 3.16e+03
KIM187 PROTEIN 3.16e+03
CHROMOSOME XY READING 3.16e+03
HYPOHETICAL 151.9 KD 3.16e+03
PRENATAL STORAGE CLIC 3.16e+03
P7B12.4. 3.16e+03
90K-PROTEASE (BACILLUS) 3.16e+03
NUCLEAR RECEPTOR COACT 3.16e+03
COSMID Y7.1. ASPARAGINE R 3.16e+03
B18A. PROTEIN. 3.16e+03
COCTEST WALL PROTEIN PR 3.16e+03
PROPHOSPHOLIPID 2. -IN 3.16e+03
DSE2. 3.16e+03
EMERSONIC MUSCLE MYOSIN 3.16e+03
ALPHA-CARDIAC MYOSIN H 3.16e+03
COILED COIL RT C. ELKMAN 3.16e+03
NUCLEAR PORE 3.16e+03
VOLUME-DEPENDENT L-TY 3.16e+03
REMOVAL CALCIUM CHAIN 3.16e+03
LCAN PROTEIN. 3.16e+03
RANODINE RECEPTOR HOM 3.16e+03

RESULT 3
ID 015533 PRELIMINARY: PRT: 50 M.
AC 015533
DT 01-JAN-1998 (TREMBLIER, 05, CREATED)
DT 01-JAN-1998 (TREMBLIER, 07, LAST SEQUENCE UPDATE)
DE 1-NOV-1996 (TREMBLIER, 01, LAST ANNOTATION UPDATE)
OC ETHYRIA, PRIMATES
GN VIA SAPIENS (HUMAN)
RA SHARON F., DOAN L., END N., BLAGERA O., POWERANTE R.J.
RM MEDLINE 9621146
RL EMBL 148716: G2289026
DR EMBL 148716: G2289026
SQ SEQUENCE 262 AA: 27842 MW: 4724086 CMC32;
KX RNA-DIRECTED DNA POLYMERASE
KW RNA-DIRECTED DNA POLYMERASE
NC

ALIGNMENTS

DAGSHUND VARIANT 2. 3.16e+03
DAGSHUND VARIANT 1. 3.16e+03
P-TYPE ATPASE 2. 3.16e+03
LATS. ANTICEN. CYPOLAS 3.16e+03
PUDATIVE METL-CAN. STIR 3.16e+03
CHITIN SYNTHASE 3.16e+03
NEUROSPICIN (FRAGMENT) 3.16e+03
FILAGGRIN (FRAGMENT) 3.16e+03
KIM187 PROTEIN 3.16e+03
CHROMOSOME XY READING 3.16e+03
HYPOHETICAL 151.9 KD 3.16e+03
PRENATAL STORAGE CLIC 3.16e+03
P7B12.4. 3.16e+03
90K-PROTEASE (BACILLUS) 3.16e+03
NUCLEAR RECEPTOR COACT 3.16e+03
COSMID Y7.1. ASPARAGINE R 3.16e+03
B18A. PROTEIN. 3.16e+03
COCTEST WALL PROTEIN PR 3.16e+03
PROPHOSPHOLIPID 2. -IN 3.16e+03
DSE2. 3.16e+03
EMERSONIC MUSCLE MYOSIN 3.16e+03
ALPHA-CARDIAC MYOSIN H 3.16e+03
COILED COIL RT C. ELKMAN 3.16e+03
NUCLEAR PORE 3.16e+03
VOLUME-DEPENDENT L-TY 3.16e+03
REMOVAL CALCIUM CHAIN 3.16e+03
LCAN PROTEIN. 3.16e+03
RANODINE RECEPTOR HOM 3.16e+03

DB 2 TFGGTR 8
117 TFGGTR 123

RESULT 27 PRELIMINARY: PRT: 109 AA.
ID Q3537: 117 TFGGTR 123
DT 01-JUN-1998 (TREMBLIER, 05, CREATED)
DT 01-JUN-1998 (TREMBLIER, 05, LAST SEQUENCE UPDATE)
DE LAMDA (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: RODENTIA.
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C.
RA UDA T., HIFOMI E., ISHIMARU M., MORIHARA F., ITOH T.;
RJ J. EMBL: STOREG, 83:33-34(1997).
DR PFAM: P00047, 159.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11503 MW; EC7P076C CRC32:
Query Match
Best Local Similarity 100.0%; Pred. No. 4, 854+00;
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 100 PGGGTR 106
OY 118 PGGGTR 124

RESULT 28 PRELIMINARY: PRT: 110 AA.
ID Q92475: 118 PGGGTR 124
DT 01-FEB-1997 (TREMBLIER, 02, CREATED)
DT 01-FEB-1997 (TREMBLIER, 02, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TREMBLIER, 07, LAST SEQUENCE UPDATE)
DE ANTI-FOLATE BINDING PROTEIN (FRAGMENT).
OS HOMO SAPIENS (HUMAN).
OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RP SEQUENCE FROM N.A.
RA FICHER M., ORICI L., MEZANMANICA D., GRIFFITHS A., COLNAGHI M.I.,
RJ J. EMBL: STOREG, 83:33-34(1997).
DR PFAM: P00047, 159.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11503 MW; EC7P076C CRC32:
Query Match
Best Local Similarity 100.0%; Pred. No. 4, 854+00;
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 100 PGGGTR 106
OY 118 PGGGTR 124

RESULT 30 PRELIMINARY: PRT: 118 AA.
ID Q3586: 118 PGGGTR 124
DT 01-NOV-1996 (TREMBLIER, 01, CREATED)
DT 01-NOV-1996 (TREMBLIER, 01, LAST SEQUENCE UPDATE)
DE HOMO SAPIENS (HUMAN).
OS HOMO SAPIENS (HUMAN).
OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RP SEQUENCE FROM N.A.
RA ERMEL R.W., KENNY T.P., CHEN P.P., ROBBINS D.L.;
RJ J. EMBL: STOREG, 83:33-34(1997).
DR PFAM: P00047, 159.
FT NON_TER 118 118
SQ SEQUENCE 118 AA: 12766 MW; D2815206 CRC32:
Query Match
Best Local Similarity 100.0%; Pred. No. 4, 854+00;
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 73 LIGSLE 79
OY 93 LIGSLE 99

RESULT 31 PRELIMINARY: PRT: 121 AA.
ID Q15984: 121 LIGSLE 79
DT 01-NOV-1996 (TREMBLIER, 01, CREATED)
DT 01-NOV-1996 (TREMBLIER, 01, LAST SEQUENCE UPDATE)
DE HOMO SAPIENS (HUMAN).
OS HOMO SAPIENS (HUMAN).
OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RP SEQUENCE FROM N.A.
RA ERMEL R.W., KENNY T.P., CHEN P.P., ROBBINS D.L.;
RJ J. EMBL: STOREG, 83:33-34(1997).
DR PFAM: P00047, 159.
FT NON_TER 121 121
SQ SEQUENCE 121 AA: 12766 MW; D2815206 CRC32:
Query Match
Best Local Similarity 100.0%; Pred. No. 4, 854+00;
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 73 LIGSLE 79
OY 93 LIGSLE 99

DB 101 PGGGTR 107
OY 118 PGGGTR 124

RESULT 32 PRELIMINARY: PRT: 114 AA.
ID Q93336: 114 PGGGTR 124
DT 01-FEB-1997 (TREMBLIER, 02, CREATED)
DT 01-FEB-1997 (TREMBLIER, 02, LAST SEQUENCE UPDATE)
DE CONDOLEBERIN (CONDOLEBERIN-RELAXING PROTEIN) (GENE) (LUTHERIN).
OS TUPAIA GLIS BELANGERI (COMMON TREE SHREW).
OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: SCANDENTIA.
RP SEQUENCE FROM N.A.
RA WHITE S.A., KASTEN T.L., FERNALD R.D.;
RJ J. EMBL: STOREG, 83:33-34(1997).
DR PFAM: P00047, 159.
FT NON_TER 114 114
SQ SEQUENCE 114 AA: 12123 MW; A330904 CRC32:
Query Match
Best Local Similarity 100.0%; Pred. No. 4, 854+00;
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 6 LIGSLE 12
OY 8 LIGSLE 14

RESULT 33 PRELIMINARY: PRT: 158 AA.
ID Q48740: 158 LIGSLE 15
DT 01-JUN-1998 (TREMBLIER, 06, CREATED)
DT 01-JUN-1998 (TREMBLIER, 06, LAST SEQUENCE UPDATE)
DE HOMO SAPIENS (HUMAN).
OS HOMO SAPIENS (HUMAN).
OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RP SEQUENCE FROM N.A.
RA LAMERLIN J.E., MCCREARY P.M., SKORONSKI E., ADAMSON A.W.,
RJ J. EMBL: STOREG, 83:33-34(1997).
DR PFAM: P00047, 159.
FT NON_TER 158 158
SQ SEQUENCE 158 AA: 17635 MW; 01CPCDAB CRC32:
Query Match
Best Local Similarity 100.0%; Pred. No. 4, 854+00;
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 9 LIGSLE 15
OY 7 LIGSLE 13

RESULT 34 PRELIMINARY: PRT: 156 AA.
ID Q48740: 156 LIGSLE 15
DT 01-JUN-1998 (TREMBLIER, 06, CREATED)
DT 01-JUN-1998 (TREMBLIER, 06, LAST SEQUENCE UPDATE)
DE HOMO SAPIENS (HUMAN).
OS HOMO SAPIENS (HUMAN).
OC EUTHERIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RP SEQUENCE FROM N.A.
RA LAMERLIN J.E., MCCREARY P.M., SKORONSKI E., ADAMSON A.W.,
RJ J. EMBL: STOREG, 83:33-34(1997).
DR PFAM: P00047, 159.
FT NON_TER 156 156
SQ SEQUENCE 156 AA: 17635 MW; 01CPCDAB CRC32:
Query Match
Best Local Similarity 100.0%; Pred. No. 4, 854+00;
Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 9 LIGSLE 15
OY 7 LIGSLE 13

[illegible]

Mon Apr 19 13:23:54 1999

US-08-836-455-2.rsp

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[illegible][illegible]

Mon Apr 19 13:23:54 1995

US-08-036-455-2.rpt

Page 48

Mon Apr 19 13:21:54 1999

us-08-036-455-2.rpt

Page 33

Db 201 DIGITAL 207
07 48 DIGITAL 54

Search completed: Thu Apr 15 18:04:57 1999
Job time : 71 secs

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sequence 3, application us/08836455

general information:
applicant: chatterjee, malaya
applicant: foon, kenneth a.
applicant: chatterjee, sunil k. . .

TO: geneseqn: * Sequences: 240,622 Total-length: 94,065,609 April 18, 1999 22:14

Database Release Information:

Geneseq-NA, Release 34.4, Released on 4Feb1999, Formatted on 5Feb1999

Word-size: 15 Words: 70791 Diagonals: 2,313 Total-diagonals: 409,502,538
Integral-width: 1 Alphabet: 4 List-size: 50 CPU minutes: 30.25

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GENESON:N91146	+	38	288	1	2H7 Vh sequence. Polynucleotide(s) en
GENESON:T51042	+	71	288	1	Coding sequence for heavy chain variab
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GENESON:T36316	+	70	288	1	2H7 antibody heavy chain variable reg
GENESON:T70868	+	71	288	1	2H7 heavy chain variable sequence. Se
GENESON:N70971	+	39	245	2	2H7 VH sequence which contains JH1 se
GENESON:065631	+	0	215	1	Murine variable region heavy chain fr
GENESON:065629	+	239	215	1	Vector contg. TCAE 8 DNA. Treating B
GENESON:062957	+	9	163	1	Anti-influenza N10 scfv. New target-h
GENESON:T35051	+	0	157	1	Mab VIL76 heavy chain (specific for
GENESON:N91645	+	63	149	1	Heavy chain of monoclonal antibody 6A
GENESON:066846	+	0	142	1	Sequence encoding the heavy chain var
GENESON:004695	+	38	139	1	Heavy chain variable domain of human
GENESON:Q12637	+	40	134	1	Monoclonal antibody OK3T heavy chain
GENESON:V54863	+	8	134	1	Murine antibody ICR-1.1 heavy chain
GENESON:V56413	+	8	134	1	Murine ICR-1.1 V-H region PCR product
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GENESON:T39557	+	60	127	1	Variable heavy chain cDNA for anti-hu
GENESON:T69541	+	60	127	1	Anti-human FasL antibody (NOK5) heavy
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GENESON:T77139	+	45	119	1	Single chain antigen hybrid receptor
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GENESON:T88129	+	57	114	1	Variable heavy chain of Mab LL2 DNA.
GENESON:V00687	+	54	114	1	Fusion gene sequence encoding anti-Ta
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GENESON:038877	+	0	110	1	CTMO1 VH cDNA. Anti-human milk fat gl
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GENESON:T58328	+	131	109	1	Ber-H2 heavy gamma chain. DNA mols.
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GENESON:073678	+	312	109	1	Fv(GP-2) immunosuppressive. Immunosu
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GENESON:V09805	+	12	105	1	DNA encoding the heavy chain of the c
GENESON:015164	+	0	104	1	VH186 region of anti-nitrophenylacety
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of sequences containing matches at least 15 nt long

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PN M09J11025-1.
PD 16-MAY-1994.
PR 11-NOV-1993; DS-170891.
PR 03-NOV-1993; DS-149099.
PA (IDC-1) IDCC PHARM COMP.
P1 Anderson DR, Hanna M, Leonard JE, Newman RA, Ratcliffe WB;
P2 WPI: 94-183162-722.
PT Treating B cell lymphoma with chimeric antibody - agalinate CD20.
PT Treating B cell lymphoma with chimeric antibody - agalinate CD20.
PT Antibodies and hypoxanthine.
PT Antibodies and hypoxanthine.
CC The sequence above a vector conty. T0C68, a gene encoding a chimeric
CC anti-CD20 antibody for treatment of B cell lymphomas. T0C68
CC contains 4 transmembranal cassettes, human Ig light and heavy chain
CC and murine variable regions. The vector can be used to produce
CC antibodies which cause depletion of peripheral blood B cells.
CC Including those associated with lymphoma. They mediate complement-
CC dependent cytotoxicity and lyses target cells by antibody-dependent cellular
CC Sec also 065829-35.
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DC T15377.
DT 25-JUN-1996 (first entry)
PR 25-JUN-1996; DS-180457.
PR 28-JUN-1994; DS-217644.
PR 03-NOV-1993; DS-149099.
P1 Gorski MB, Reisel MG;
P2 WPI: 96-077494/08.
DR P-PS08: R09081.

[illegible]

Mon Apr 19 13:23:56 1999

US-08-036-455-3.png

Page 67

Mon Apr 19 13:23:56 1995

U8-08-036-455-3.png

Page 68

[illegible]

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PR AC Q38745.1; NC_007111.1
PR 24-NOV-1993; US-039457.
PR 22-APR-1993; US-039457.
P PR1 J NESTIN SHOWN IN KATUNA LTD.
P P1 NP_054119.1/10.
DR P-SPB8: R46813.
DR WP001: 40759.94 T.
PT New humanized antibody specific for epitope on HIV-1 gp 120 -
PT able to neutralize infection of He cells, also nucleic acid
PT RTV-1 infection.
PT RTV-1 infection.
PS Env-1: Page 41-42, 91bp; English.
CC GPCR is a portion of HIV-1 gp120 or gp160 protein. Monoclonal
CC to neutralize the infection of He cells and which has the capacity
CC to neutralize the infection of He cells and which has the capacity
CC streptin NR and IIB are claimed. Specifically illustrating the
CC invention are the murine MB 10726 which is deposited under ATCC HB
CC hybridoma cell line HB 10726 which is deposited under ATCC HB
CC 10726, the murine MB 10726 cytoplasmic RNA as template. The DNA was
CC then sequenced. The DNA and deduced AA sequences are given in
CC 1bp chains of MB-NR-01 were cloned by PCR using cDNA generated
CC from hybridoma HB 10726 cytoplasmic RNA as template. The DNA was
CC then sequenced. The DNA and deduced AA sequences are given in
CC CC Q56655 correspond to the PCR primers used to amplify the MB-01-light
CC chain sequences and nucleotides 1-27 and 385-403 of Q56655 corresp-
CC to PCR primers used to amplify MB-01 heavy chain sequences.
CC Resequencing the variable regions of MB-Q56655 identified in the
CC sequence 402 bp; 106 A; 113 C; 89 G;
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db 338 tactcgggtctacgaagaccatccatcgatcccttcctccatgcaaac 371
QY 376 tttcccgccttcaaaactccaacccaaaccccccccccccccccccccc
RESULTS 16 standard. DNA: 417 BP.
D7 01-MAR-1993 (first entry)
D7 anti-CD4 specific heavy chain variable region DNA.
D7 NM region: diagnostic; tumour markers; lymphocyte; ap.
Key keyword Location/Qualifiers

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Search completed: Sat Apr 17 17:44:14 1999
Job time : 271 secs.

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(Nucleotide) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-3 check: 9532 from:

FROMIG of: /home/obryen/ree455/olig/us-08-836-455-3
sequence 3, application us/08836455

general information:

applicant: chatterjee, malaya
applicant: toon, kenneth a.
applicant: chatterjee, sunil k. . .

TO: GenEMBL: * Sequences: 602,539 Total-length: 1,199,477,030 April 18, 1999 21:41

Database Release Information:

GenBank, Release 110.0, Released on 14Dec1998, Formatted on 15Dec1998
EMBL, Release 56.0, Released on 16Sep1998, Formatted on 15Dec1998

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Integral-width: 1 Alphabet: 4 List-size: 50 CPU minutes: 118.14

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GB_PAT:108811	+	38	288	1	108811 Sequence 12 from Patent WO 880
GB_PAT:105921	+	38	288	1	105921 Sequence 37 from Patent EP 027
GB_RO:MUSIGHXW	+	38	288	1	M17953 Mouse Ig rearranged H-chain V-
GB_RO:MMAIDHCH	+	-57	240	1	X64805 M.musculus mRNA for anti-id m
GB_RO:MUSY	+	-57	237	1	L48668 Mus musculus (cell line C3H/F2
GB_SY:XXU49832	+	375	233	1	U49832 Synthetic single chain Fv anti
GB_RO:MMMD01C	+	-57	230	1	273357 M.musculus mRNA for rearranged
GB_RO:MMMD52C	+	-57	230	1	273358 M.musculus mRNA for rearranged
GB_RO:MMIGGCVRI	+	-57	230	1	225457 M.musculus immunoglobulin gam
GB_RO:MMIGGCVRE	+	-57	230	1	225449 M.musculus immunoglobulin gam
GB_RO:MMIGGCVRD	+	-57	230	1	225447 M.musculus immunoglobulin gam
GB_RO:MMIGGCVRG	+	-78	228	1	225453 M.musculus immunoglobulin gam
GB_RO:MMIGGCVRF	+	-78	228	1	225451 M.musculus immunoglobulin gam
GB_RO:MMIGGCVRC	+	-78	228	1	225445 M.musculus immunoglobulin gam
GB_RO:MMIGGCVRB	+	-78	228	1	225443 M.musculus immunoglobulin gam
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GB_PAT:AR015961	+	2400	215	1	AR015961 Sequence 2 from patent US 57
GB_PAT:AR000013	+	0	215	1	AR000013 Sequence 9 from patent US 57
GB_RO:AF025445	+	650	214	1	AF025445 Mus musculus clone BHS2.19
GB_RO:MMMD47C	+	-57	214	1	273342 M.musculus mRNA for rearranged
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GB_RO:MMUL7HC	+	-100	194	1	272457 M.musculus mRNA for immunogl
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GB_RO:MUSIGHAAN	+	54	148	1	M19897 Mouse Ig rearranged gamma-chai
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GB_RO:MUSIGZM5	+	226	143	1	D14634 Mouse embryo DNA for immunogl
GB_RO:S45115	+	49	143	1	S45115 Ig VDJ H (active allele) [mice
GB_SY:XXU44796	+	-57	140	1	U44796 Synthetic construct single-ch
GB_PAT:A07953	+	38	139	1	A07953 Artificial sequence for anti-h
GB_RO:MMIGVAP	+	-76	139	1	222064 M.domesticus IgG variable regi
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not all containing matches at least 15 nt long

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Physiologist, Department of Medical and Physiological Chemistry,
Hastings 3, Uppsala, 75123, Sweden
REFERENCE
3 (bases 1 to 303)
AUTHORS
Mo, J. A., Bona, C. A., and Holmblad, R.
TITLE
Variable region gene selection of immunoglobulin C-expressing B
cells with specificity for a defined epitope on type II collagen
JOURNAL
Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE
94009207
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Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DEFINITION
Mammalian immunoglobulin gamma heavy chain (DBM/1) gene, V region.
ACCESSION
U08848
KEYWORDS
heavy chain; 196 gene; immunoglobulin; variable region.

Db 41 CTGGGCTTACGAGATTCCTGACAGGCTTCGACACATTCACATTCACATTA 100
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DEFINITION
Mammalian mRNA for rearranged Ig heavy chain V region (J588
family; 129MD.50c).
ACCESSION
U08848
KEYWORDS
heavy chain; immunoglobulin superfamily; joining region; variable
region.
SOURCE
house mouse.
ORGANISM
Mus musculus; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE
1 (bases 1 to 353)
AUTHORS
Gilliland, S., Fujisawa, H., Kikuchi, H., Kuhn, R., Rose, J., Muller, M.,
Gilliland, S., Fujisawa, H., Kikuchi, H., Kuhn, R., Rose, J., Muller, M.,
Benoist, C., Wehler, D., Kishimoto, T., Mak, T. W., and Rajeswari, K.
TITLE
Somatic hypermutation occurs in B cells of Td, CD23, IV-4, 19D and
CD30 deficient mouse mutants
JOURNAL
Eur. J. Immunol. 26 (8), 1966-1969 (1996)
MEDLINE
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ACCESSION
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KEYWORDS
heavy chain; immunoglobulin superfamily; joining region; variable
region.
SOURCE
house mouse.
ORGANISM
Mus musculus; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE
1 (bases 1 to 353)
AUTHORS
Gilliland, S., Fujisawa, H., Kikuchi, H., Kuhn, R., Rose, J., Muller, M.,
Gilliland, S., Fujisawa, H., Kikuchi, H., Kuhn, R., Rose, J., Muller, M.,
Benoist, C., Wehler, D., Kishimoto, T., Mak, T. W., and Rajeswari, K.
TITLE
Somatic hypermutation occurs in B cells of Td, CD23, IV-4, 19D and
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JOURNAL
Eur. J. Immunol. 26 (8), 1966-1969 (1996)
MEDLINE
94009207
FEATURES
Location/Qualifiers
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Physiologist, Department of Medical and Physiological Chemistry,
Hastings 3, Uppsala, 75123, Sweden
REFERENCE
3 (bases 1 to 303)
AUTHORS
Mo, J. A., Bona, C. A., and Holmblad, R.
TITLE
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cells with specificity for a defined epitope on type II collagen
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Eur. J. Immunol. 23 (10), 2503-2510 (1993)
MEDLINE
94009207
FEATURES
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Matches 106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 41 CTGGGCTTACGAGATTCCTGACAGGCTTCGACACATTCACATTCACATTA 100
QY 98 CTGGGCTTACGAGATTCCTGACAGGCTTCGACACATTCACATTCACATTA 157
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QY 158 TCCACTGGCTTAACGACACCTGACAGGCTTCGACACATTCACATTCACATTA 204
RESULT 14 MHC/CYT 105 bp RNA ROD 20-DEC-1996
DEFINITION
Mammalian mRNA for rearranged Ig heavy chain V region (J588
family; 129MD.47c).
ACCESSION
U08848
KEYWORDS
heavy chain; immunoglobulin superfamily; joining region; variable
region.
SOURCE
house mouse.
ORGANISM
Mus musculus; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Mus.
REFERENCE
1 (bases 1 to 353)
AUTHORS
Gilliland, S., Fujisawa, H., Kikuchi, H., Kuhn, R., Rose, J., Muller, M.,
Gilliland, S., Fujisawa, H., Kikuchi, H., Kuhn, R., Rose, J., Muller, M.,
Benoist, C., Wehler, D., Kishimoto, T., Mak, T. W., and Rajeswari, K.
TITLE
Somatic hypermutation occurs in B cells of Td, CD23, IV-4, 19D and
CD30 deficient mouse mutants
JOURNAL
Eur. J. Immunol. 26 (8), 1966-1969 (1996)
MEDLINE
94009207
FEATURES
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Murinae; Mus.
REFERENCE 1 (bases 1 to 390)
AUTHORS Lohman K.L., Buck D.W., Carrillo M.A. and Kennedy R.C.
TITLE Characterization of murine monoclonal anti-CD4: epitope
JOURNAL Immunology 71:105-112 (1992)
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DEFINITION MHC11TCGV 414 bp mRNA ROD 02-OCT-1997
ACCESSION 92459928
KEYWORDS V-region, immunoglobulin heavy chain
SOURCE Human
ORIGIN
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Murinae; Mus.
REFERENCE 1 (bases 1 to 414)
AUTHORS Lohman K.L., Buck D.W., Carrillo M.A. and Kennedy R.C.
TITLE Characterization of murine monoclonal anti-CD4: epitope
JOURNAL Immunology 71:105-112 (1992)
FEATURES
source 1. 414
/organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="SP20-BALB/c fusion hybridoma"
/feature="CD4"
/gene="IGH"
/note="protein sequence is in conflict with the conceptual
translation."
BASE COUNT 98 a 100 c 102 g 90 t
ORIGIN

Query Match 13.8% Score 59; DB 29; Length 414;
Best Local Similarity 100.0%; Pred No. 237e-37;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 314 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 372
QY 371 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 429

RESULT 29 MHC11TCGV 410 bp mRNA ROD 23-MAR-1995
LOCUS MHC11TCGV 410 bp mRNA ROD 23-MAR-1995
DEFINITION Mouse mAb-15C5 mRNA for immunoglobulin gamma-1 chain V-CH1
ACCESSION X56192
KEYWORDS V-region, immunoglobulin heavy chain
SOURCE Human
ORIGIN
Eukaryotes; mitochondria; eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae;
Murinae; Mus.
REFERENCE 1 (bases 1 to 410)
AUTHORS Vandamme A.M.I.
TITLE Subcloned (05-JUN-1990) Vandamme A.M.I., University of Leuven,
Center for Thrombosis and Vascular Research, Herestraat 49, B-3000
Leuven

Query Match 13.8% Score 59; DB 29; Length 414;
Best Local Similarity 100.0%; Pred No. 237e-37;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 314 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 372
QY 371 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 429

Query Match 13.8% Score 59; DB 29; Length 390;
Best Local Similarity 100.0%; Pred No. 237e-37;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 320 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 378
QY 371 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 429

RESULT 27 A18395 401 bp RNA RAT 26-MAR-1994
LOCUS Human uPA cDNA
DEFINITION A18395
ACCESSION 9512444
KEYWORDS uPA
SOURCE Human
ORIGIN
Eukaryotes; mitochondria; eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Rodentia; Homo.
REFERENCE 1 (bases 1 to 401)
AUTHORS THROMBUS-SPECIFIC ANTIBODY DERIVATIVES
TITLE
JOURNAL Patent: WO 91/03533-A 31 31-OCT-1991.
FEATURES
source 1. 401
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="P18781"
/gene="uPA"
/note="protein sequence is in conflict with the conceptual
translation."
BASE COUNT 112 a 102 c 91 g 96 t
ORIGIN

Query Match 13.8% Score 59; DB 29; Length 401;
Best Local Similarity 100.0%; Pred No. 237e-37;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 310 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 368
QY 371 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 429

Query Match 13.8% Score 59; DB 29; Length 401;
Best Local Similarity 100.0%; Pred No. 237e-37;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 310 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 368
QY 371 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 429

Query Match 13.8% Score 59; DB 29; Length 401;
Best Local Similarity 100.0%; Pred No. 237e-37;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 310 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 368
QY 371 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 429

Query Match 13.8% Score 59; DB 29; Length 401;
Best Local Similarity 100.0%; Pred No. 237e-37;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 310 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 368
QY 371 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 429

Query Match 13.8% Score 59; DB 29; Length 401;
Best Local Similarity 100.0%; Pred No. 237e-37;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 310 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 368
QY 371 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 429

Query Match 13.8% Score 59; DB 29; Length 401;
Best Local Similarity 100.0%; Pred No. 237e-37;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 310 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 368
QY 371 TCGACCTACGCGTAAAGAACTGATGACGCTCTCTGACCAAGACAGCCCA 429

[illegible][illegible]

```

CC FT misc_feature 226. .321 /note=Fragment 3 of heavy chain variable
CC FT 327 idios 327 /note=idios
CC FT misc_feature 328 50 /note=CDR3 of heavy chain variable region of
CC FT 329 idios 329 /note=idios
CC FT 330 idios 330 /note=Fragment 4 of heavy chain variable
CC FT 331 idios 331 /note=idios
CC FT Key Location/Qualifiers
FH Key 1..339 /organism="Mus musculus"
FT source
SQ Sequence 399 BP; 106 A; 102 C; 105 G; 86 T; 0 other;
SQ 14% Score 57; DB 10; Length 399;
Query Match Similarity 100.0%; Pseq. No. 2,806-35;
Beat Local Conservative 0; Mismatch 0; Indels 0; Gap
Matches 57;
db 343 CTGACATCTGGGGCGAGCAAGCAGTGCAGTCCTGTCTCATGCCNNNNNCAACACC 399
370 CTCGACATCTGGGGCGAGCAAGCAGTGCAGTCCTGTCTCATGCCNNNNNCAACACC 426

```

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REFERENCE 1 (bases 1 to 433)
 AUTHORS Hiltner, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Roman, M., Rutman, M., Rucaba, T., Le, M., Lennon, G., Morris, M., Trevisan, J., Ruffin, L., Rohlfing, T., Soares, M., Tan, F., Wilson, R., Waterston, R., Williamson, A., Woldmann, P., and Wilson, R.
 The WashU-Herx EST Project
 Unpublished (1995)

TITLE 3181L
 JOURNAL
 COMMENT

FEATURES
 source

BASE COUNT 149 a 80 c 65 g 139 t
 ORIGIN

Query Match 4.3% Score 20; DB 19; Length 433;
 Best Local Similarity 100.0%; Pred. No. 3.62e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 357 TACATGACAGTTAGG 376
 235 TACATGACAGTTAGG 254

RESULT 8
 LOCUS A116128 552 bp mRNA EST 14-MAY-1997
 DEFINITION 253199.11 Sources pregnant uterus NBRU Homo sapiens CDNA clone
 PRECUNSOR (HMAN), mRNA sequence.
 ACCESSION A116128
 ID 91671177
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae;

CP 188 CCTCTCCAGCTCTCTT 169

RESULT 9
 LOCUS H47534 478 bp mRNA EST 16-AUG-1995
 DEFINITION YP78409.F1 Homo sapiens CDNA clone 193515.5 similar to
 SP-EST, CAMEL P23691 ELONGATION FACTOR 2.
 ACCESSION 9293586
 ID 9293586
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Eumetazoa; Bilateria; Coelomata;
 Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 478)
 AUTHORS Hiltner, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Roman, M., Rutman, M., Rucaba, T., Le, M., Lennon, G., Morris, M., Trevisan, J., Ruffin, L., Rohlfing, T., Soares, M., Tan, F., Wilson, R., Waterston, R., Williamson, A., Woldmann, P., and Wilson, R.
 The WashU-Herx EST Project
 Unpublished (1995)

TITLE 3181L
 JOURNAL
 COMMENT

FEATURES
 source

BASE COUNT 95 a 134 c 123 g 120 t 6 others

REFERENCE 1 (bases 1 to 552)
 AUTHORS Hiltner, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Roman, M., Rutman, M., Rucaba, T., Le, M., Lennon, G., Morris, M., Trevisan, J., Ruffin, L., Rohlfing, T., Soares, M., Tan, F., Wilson, R., Waterston, R., Williamson, A., Woldmann, P., and Wilson, R.
 The WashU-Herx EST Project
 Unpublished (1995)

TITLE 3181L
 JOURNAL
 COMMENT

FEATURES
 source

BASE COUNT 123 a 167 c 142 g 117 t 3 others

Query Match 4.3% Score 20; DB 6; Length 552;
 Best Local Similarity 100.0%; Pred. No. 3.62e-08;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 354 CCTCTCCAGCTCTCTT 373

ORIGIN
 Query Match 4.1% Score 19; DB 16; Length 478;
 Best Local Similarity 100.0%; Pred. No. 2.12e-06;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 353 GGGCCCTCCAGCTCTT 370
 100 GGGCCCTCCAGCTCTT 118

RESULT 10
 LOCUS A488443 208 bp mRNA EST 27-MAY-1998
 DEFINITION 3516108.1 Sources testis NBRU Homo sapiens CDNA clone 1394774
 similar to TR:008810 008810 05-118ED. mRNA sequence.
 ACCESSION 92893983
 ID 92893983
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryote; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
 Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 208)
 AUTHORS NCI-CCRP http://www.ncbi.nlm.nih.gov/ncicgsp.
 NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Unpublished (1997)

TITLE 3181L
 JOURNAL
 COMMENT

FEATURES
 source

BASE COUNT 95 a 134 c 123 g 120 t 6 others

NID 62708434
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum
ORGANISM Mesembryanthemum crystallinum
REFERENCE Cushman, J.C. 1997. Sequence tag database for the common ice plant, Mesembryanthemum crystallinum. Unpublished (1997).
AUTHORS Cushman, J.C.
TITLE Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT

Contact: Cushman JC
Department of Chemistry and Molecular Biology
Oklahoma State University
350 Noble Research Center, Stillwater, OK 74078-3035, USA
Tel: 405-744-6207
Fax: 405-744-6207
E-mail: jcs@okstate.edu
PER Palatka
FORWARD: 77
REMARKS: 77
BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

BASE COUNT 140 A 106 G 138 C
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Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

NID 62708434
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum
ORGANISM Mesembryanthemum crystallinum
REFERENCE Cushman, J.C. 1997. Sequence tag database for the common ice plant, Mesembryanthemum crystallinum. Unpublished (1997).
AUTHORS Cushman, J.C.
TITLE Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
COMMENT

Contact: Cushman JC
Department of Chemistry and Molecular Biology
Oklahoma State University
350 Noble Research Center, Stillwater, OK 74078-3035, USA
Tel: 405-744-6207
Fax: 405-744-6207
E-mail: jcs@okstate.edu
PER Palatka
FORWARD: 77
REMARKS: 77
BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

NID 62708434
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum
ORGANISM Mesembryanthemum crystallinum
REFERENCE Cushman, J.C. 1997. Sequence tag database for the common ice plant, Mesembryanthemum crystallinum. Unpublished (1997).
AUTHORS Cushman, J.C.
TITLE Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
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Department of Chemistry and Molecular Biology
Oklahoma State University
350 Noble Research Center, Stillwater, OK 74078-3035, USA
Tel: 405-744-6207
Fax: 405-744-6207
E-mail: jcs@okstate.edu
PER Palatka
FORWARD: 77
REMARKS: 77
BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

NID 62708434
KEYWORDS EST.
SOURCE Mesembryanthemum crystallinum
ORGANISM Mesembryanthemum crystallinum
REFERENCE Cushman, J.C. 1997. Sequence tag database for the common ice plant, Mesembryanthemum crystallinum. Unpublished (1997).
AUTHORS Cushman, J.C.
TITLE Mesembryanthemum crystallinum
JOURNAL Unpublished (1997)
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Department of Chemistry and Molecular Biology
Oklahoma State University
350 Noble Research Center, Stillwater, OK 74078-3035, USA
Tel: 405-744-6207
Fax: 405-744-6207
E-mail: jcs@okstate.edu
PER Palatka
FORWARD: 77
REMARKS: 77
BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

BASE COUNT 140 A 106 G 138 C
ORIGIN
Query Match 3.9%; Score 18; DB 11; Length 474;
Best Local Similarity 100.0%; Pctd. No. 1.05e-04;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 333 TTTTCCGCAAAATCGCA 340
QY 210 TTTTCCGCAAAATCGCA 227

Emmett-Shuck, M. D., Ph.D.,
Ph.D. Library Preparation: Strategene, Inc., David B. Kitzman,
CGMA Library Arraying: Greg Lannon, Ph.D.,
CGMA sequencing by: Washington University Genome Sequencing Center
found through the I.M.A.E. Consortium/IMB at:
web:bio.illinois.gov/ibmb/lange.html
Insert Length: 1756 std Error: 0.00
Seq primer: -40ml1 fwd Rr from Amerham
High quality: 100%
Location/Qualities:
1. 696

mrna	<1.	>696	
BASE COUNT	176 a	166 c	197 g 157 t
ORIGIN			

```

Query Match Score 18: 3.9% DB 9: Length 696:
Best Similarity 100.0%
Pred No. 1.05e-04:
Matches 18: Conservative 0: Mismatches 0: Indels 0: Gaps 0
Db 434 ACACCTCCACACGAGCCG 431
|||||
Cp 118 ACACCTCCACACGAGCCG 101

```

DEFINITION		MHSN	EST	09-JUN-1999
ACCESSION	AI00101 at GenBank			
IMAGE	16912818.tif			
SEQUENCE				
NID	93203061			
KEYWORDS				
EST.				
SOURCE	Human			
TISSUE	Brain, Cerebellum			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria			
	Pekaryota; Catarrhini; Hominoidea; Homo.			

DEPOS	AG159606	745 bp	DNA	GSS	08-SEP-1998				
DEFINITION	gms00000101orf_c001, right blast, BAC Library Magnaporthe grisea spores								
ACCESSION	AG159606								
VERSION	gms00000101orf_c001, genomic survey sequence.								
KEYWORDS	gms00000101orf_c001								
ORGANISM	Magnaporthe grisea.								
REFERENCE	1. base(s) 1 to 745								
AUTHORS	Yu, Y.; Zhu, H.; Boyd, C.A.; Gaudette, B.; Gayle, A.; Kingsbury, R.; Phillips, K.; Saitonowski, M.; Wang, R.A. and Dean, R.A.								
TITLE	A BAC Map Sequencing Framework to Sequence the Magnaporthe grisea Genome								
JOURNAL	Unpublished (1998)								
COMMENT									

Clemson University, Genomics Institute
 100 Jordan Hall, Clemson University, Clemson, SC 29634
 Tel: 864 656 5737
 Fax: 864 656 5293
 Email: clg@clg.clemson.edu
 Seq primer: GGAAGACCTATGACCATG
 Class: BAC ends
 High qual: 1
 Sequence stop: 435
 Locat: 1
 Source: 1, 745

Rice blast is one of the most important diseases of rice world wide. It is a filamentous ascomycete caused by *Magnaporthe oryzae*. A haploid genome (~70 Mb) of approximately 40 kbp. Rice has been sequenced by the International Rice Genome Sequencing Project. In order to facilitate genome wide analysis, a BAC library of rice was constructed along with an average insert size of 130 kb. The library contains 60,000 clones with an average coverage of 7x per genomic region. High density colony filters are available upon request.

```

BASE COUNT      213 a      161 c      177 g      189 c      5 others
ORIGIN
Query Match      3.9%  Score 18;  D8 20;  Length 745

```

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 73)	Hillier, L., Allen, M., Boyes, L., Dubnue, T., Castej, G., Jose, S., Kitzman, D., Knuch, P., Lacy, M., Le, N. T., Leung, Y., Ma, H., Martin, J., Moor, B., Schellderm, S., Stephens, R., Wain, P., Williams, B., White, Y., Wylie, T., Watson, R. and Wilson, R.	Maand-NCI human EST Project	Unpublished (1997)	

Contact: Milton R. K...by School of Medicine
 4444 Forest Park Parkway, Box 9501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 This close relation must edu
 IMAC Corporation (IndoAnglo Intl) poss
 Possible reversed close relation on wrong strand
 seq primer: 43m3 fwd. 5' from Arabzham
 H50.4
 Location/Qualifiers
 1..738
 source

[illegible]

```

Mon Apr 19 11:21:57 1999

                                US-01-036-455-3.ent

RESULT      43

Best Local Similarity 100.0%;  Pred. No. 1.05e-04;
Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Db      481  GCGAGCTGCGGCTGAGCT 498
          |||.....|
07      72  GCGAGCTGCGGCTGAGCT 89

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RESULT 44
 LOCUS A443368 167 bp
 DEFINITION M44305.1 h1 MCI.CAP.G63. mRNA
 ACCESSION A44348
 MID G1872181
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Tissue: bone marrow
 Vector: pTZ19
 Vertebrate: Vertebrate
 Mammalian: Mammalian
 Reptiles: Reptiles
 Primates: Primate
 Carnivora: Carnivora
 Rodentia: Rodentia
 Insecta: Insecta
 Chordata: Chordata
 Eukaryotes: Eukaryotes
 Metazoa: Metazoa
 Reference: 1 (bases 1 to 167)
 MCI.CAP http://www.ncbi.nlm.nih.gov/ncisg.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997)

Contact: Robert Strunberg, Ph.D.
 Tel.: (301) 498-1150
 Fax: (301) 498-1150
 Email: robert.strunberg@nih.gov
 This clone is available through INM; contact the
 INMCG Consortium (info@inm1.gov) for further information.
 Insert Length: 1531 bp
 Bid Error: 0.00
 High quality: 98%
 Read: 12727
 Read Error: 0.00
 High quality: 98%
 Read: 12727
 Location/Qualities
 1. 167

[illegible]

REFERENCE

1. (pages 1 to 738)

Kirkman D., Wilson R., Boyles J., Dubnue T., Gelst G., Jose S.

Mattain J., Moore M., Schellinger K., Stepan N., Tan H.

Wahlberg L., Williams T., Willett W., Watson R. and Wilson R.

Unpublished (1997) "Project"

TITLE

JOURNAL

COMMENT

Contact: Wilson R.
Washington University School of Medicine
744 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810

RNA was prepared by acid-phenol, followed by oligo dT selection. cDNA library prepared by the BRL/Life Tech. Superscript Plasmid system. oligo-dT NotI primer for first strand synthesis.

[illegible]

```

ORIGIN      1
Query Match      3 99:      Score 18:  DN 15:      Length 738:
Best Local Similarity 100.00:
Matches 18:      Conservative 0:      Mismatches 0:      Indels 0:      Gaps 0:
Db 437      ACACCTCCTACCTACGCC 454
      |||||
CP 118      ACACCTCCTACCTACGCC 101

```

[illegible]

Eukaryotic, Mitochondrial, eukaryotic, Metazoan, Chordates,
 Vertebrates, Vertebrata, Euteleostomi, Placentalia, Homi-
 nidae, 1 (base 1 to 167)
 NCBI-Genbank <http://www.ncbi.nlm.nih.gov/ncbi/gp>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Unpublished (1997).
 Contact: Robert Steinberg, Ph.D.
 Tel.: (301) 495-1551

```

HIGH QUALITY SEQUENCE (info:seqs.info.gov) for further information.
Seq primer: small_1064.fwd Error: 0.00
Seq primer: small_1064.rev Error: 0.00
High quality sequence stop: 143.
Location/Qualifier
1
/organs/Homo sapiens/
/note=Vector: pY7D-Pac (Pharmacia) With a modified
CDNA from rat liver tissue. Eco RI: 1st strand
was disrupted from 5' end. Bam HI: 1st strand
genomic center B cuts by 1100 bp (C202+).
Eco RI: 1st strand

```

3). Double-stranded cDNA was ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not and Eco RI sites of the modified p773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonardo.*

[illegible]

```

TITLE      JOURNAL
SOURCE     Contract Venter, JC
           The Institute for Genomic Research
           9310 Clopper Rd., Gaithersburg, MD 20878
           Tel.: 3016569221
           Fax : 3016569423
           Email: cdbs@icr.edu; tigr.org
           For clone availability, additional sequence and expression
           information related to this EST, please contact the TIGR database
           administrator at location/Qualifiers
FEATURES   1..209 /organism=Homo sapiens+
source                                           +
ORIGIN     mRNA
BASE COUNT    43 A... 62 G... 48 G... 55 C... 1 others
Query Match          Score 17, DB Size Length 209,
Best Local Similarity 100.0% , Gap 0:
Matches 17: Conservative 0; Mismatched 0; Indels 0; Gaps 0;
Db       150 CGACAGACTTCGACA 166
            |||.....|||.
Cp       134 CCAGAACCTTCCAGA 118
            |.|.....|.
RESULT  #?  T39660        238 bp, mRNAs, EST#         06-SEP-1995
LOCUS       ES289587 Homo sapiens cDNA 5' end similar to immunoglobulin heavy
DEFINITION Chitin Y region (GB:U61013) (MT:3210).
ACCSSION   U611166
MOL ID     EST#
KEYWORDS   human, primer-M13 Reversease Library-Human Small intestine.
ORGANISM   Mus musculus [Mus], Mussetosa; Blastarici; Coelomata;
           Euteleostomi; Choradai; Vertebrate; Chordatescomata; Osteichthyes;
           Sarcopterygii; Chondaria; Tetrapoda; Amniota; Mamalia; Theria;
           Placentalia; Artiodactyla; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE  Bullock,C.Y., Lee,M.H., Kikuchi,E.F., Weinstock,R.C., Goddard,J.D.,
AUTHORS     White,O., Sutton,G., Blake,C.A., Brandon,K.R., Chiu,W.W.,
           Clayton R.A., Clifton,N.D., Earlie-Hughes,P., Fine,L.D.,

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[illegible]

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FROMIG of: /home/obryen/tee455/olig/us08836455.pep
sequence 4, application us/08836455

general information:

applicant: chatterjee, malaya

applicant: foon, kenneth a.

applicant: chatterjee, sunil k. . .

TO: geneseqp: * Sequences: 162,890 Total-Length: 20,225,328 April 18, 1999 14:16

Database Release Information:

Geneseq-AA, Release 34.4, Released on 4Feb1999, Formatted on 5Feb1999

Word-size: 5 Words: 72204 Diagonals: 6,774 Total-Diagonals: 44,984,456
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 5.18

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GENESQ:P94780	+	0	96	1	2 H7 VH gene. Polynucleotide(s) encod
GENESQ:W27122	+	-19	96	1	Murine antibody heavy chain variable
GENESQ:W10588	+	0	96	1	2H7 antibody heavy chain variable reg
GENESQ:W16343	+	0	96	1	2H7 heavy chain variable sequence. Se
GENESQ:W10242	+	0	96	1	Heavy chain variable sequence of 2H7.
GENESQ:W47520	+	0	96	1	Mouse 2H7 antibody heavy chain variab
GENESQ:W47513	+	0	96	1	Mouse 2H7 antibody heavy chain variab
GENESQ:W41070	+	0	95	1	Mouse 2H7 antibody heavy chain variab
GENESQ:P70627	+	0	95	1	Sequence encoded by the 2H7 VH sequen
GENESQ:R89004	+	0	76	1	Mab VLI7B5 heavy chain (specific for
GENESQ:R83111	+	0	74	1	Sequence of murine antibody CC46 VH.
GENESQ:R55215	+	0	72	1	Murine variable region heavy chain fr
GENESQ:R62445	+	0	71	1	81C6 heavy chain variable region. Tre
GENESQ:R04381	+	0	69	1	Variable heavy chain encoded by seq.
GENESQ:R38310	+	0	69	1	Sequence of VH-alpha-TAG New composi
GENESQ:W29750	+	0	67	1	Anti-HMFg Mab CTM01 heavy chain varia
GENESQ:R13061	+	0	67	2	Monoclonal antibody OK3T heavy chain.
GENESQ:R15441	+	-19	67	1	Heavy chain variable region of Mab 18
GENESQ:W27356	+	-19	66	1	Heavy chain variable region of human
GENESQ:W27359	+	-19	66	1	Heavy chain variable region of chimer
GENESQ:R79159	+	0	65	1	Human IGE receptor-binding antibody-2
GENESQ:R05090	+	-20	65	1	Heavy chain variable domain of human
GENESQ:W19017	+	-20	65	1	Anti-human FasL antibody (NOK5) heavy
GENESQ:W00831	+	-19	65	2	Variable heavy chain of anti-human Fa
GENESQ:R79863	+	0	64	1	Anti-EGFR antibody heavy chain variab
GENESQ:R04384	+	0	64	1	Colon Cancer monoclonal antibody CC83
GENESQ:R53554	+	0	64	1	DREG-200 Ab heavy chain variable regi
GENESQ:R38313	+	0	64	1	Sequence of murine antibody CC83 VH.
GENESQ:W06213	+	0	63	1	MAB Co-1 heavy chain variable region.
GENESQ:R09425	+	0	63	2	Co-1 Heavy Chain V Region (mouse). CH
GENESQ:W07436	+	-19	63	2	Anti-DNA antibody 9f11 group heavy ch
GENESQ:R79865	+	-19	63	1	Anti-EGFR antibody heavy chain variab
GENESQ:P93151	+	0	62	1	Protein encoded by V and J regions of
GENESQ:R2184	+	-19	62	1	Murine VH group 1 chain J specific fo
GENESQ:R21281	+	-19	62	1	Murine VH group 1 chain R specific fo
GENESQ:R21279	+	-19	62	1	Murine VH group 1 chain P specific fo
GENESQ:R21264	+	-19	62	1	Murine VH group 1 chain K specific fo
GENESQ:R21273	+	-19	62	1	Murine VH group 1 chain J specific fo
GENESQ:R21274	+	-22	62	1	CTM01 VH. Anti-human milk fat globule
GENESQ:R33950	+	0	62	1	Heavy chain variable region of anti-P
GENESQ:R30014	+	2	61	1	Colon Cancer monoclonal antibody CC46
GENESQ:R04382	+	0	61	1	Colon Cancer monoclonal antibody CC46
GENESQ:P93079	+	0	61	1	Heavy chain of monoclonal antibody 6A
GENESQ:R21278	+	-19	61	1	Murine VH group 1 chain O specific fo
GENESQ:R21276	+	-19	61	1	Murine VH group 1 chain M specific fo
GENESQ:R38312	+	0	61	1	Sequence of murine antibody CC49 VH.
GENESQ:W1257	+	0	61	2	Murine antibody ICR-1.1 heavy chain a
GENESQ:W76127	+	0	61	2	Murine ICR-1.1 V-H region PCR product

of aggs containing matches of least 5aa long

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DE 03-WA-1597 (first entry)
 DE Monoclonal antibody used heavy chain variable region coding sequence.
 DE Human immunodeficiency virus type-1 (HIV-1) strain 92UG021.10.
 DE Monoclonal antibody: infection; heavy chain; light chain; hybridoma.
 DE Homo sapiens.
 DE 24-APR-1995: US-748562.
 DE 22-AUG-1991: US-748562.
 DE 24-AUG-1993: WO-007111.
 DE 24-AUG-1993: US-111080.
 DE (HSP) NISSIN SIKOKUIN KASIMA LTD.
 DE 03-WA-1597/44.
 DE Monoclonal antibodies to HIV-1, used for the prevention,
 DE treatment or diagnosis of HIV-1 infection.
 DE Example 9: Column 29-30: 56pp; English.
 DE The invention relates to a novel monoclonal antibody designated MM-01.
 DE HIV-1 strain MM. Spleenocytes from a 2-month old BALB/c mice with live
 DE cells (ATCC CRL1597). Hybridomas were screened using membrane
 DE non-infectious and HIV-infected B9 cells. By reacting with hybridoma
 DE and radiolabelled HIV-1 antigen, the antigen binding specificity of
 DE which secretes the antibody MM-01. This sequence is shown in SEQ
 DE deduced amino acid sequence of the heavy chain variable region. The final
 DE antibody obtained after resequencing the clone is shown in SEQ259. The
 DE gp130 protein (or gp160 precursor) of HIV-1 is known to only binds
 DE HIV-1 strain 1115 and MM. The antibody is used for the diagnosis of
 DE infection. 134 AA.
 DE Query Match 12.44; Score 19; DB 20; Length 134;
 DE Best Local Similarity 100.0%; Pred. No. 138e-11;
 DE Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE 109 dymgagatvvaakttpp 127
 DE 135 dymgagatvvaakttpp 143
 DE RESULT 9
 DE ID R14961 standard; Protein: 135 AA.
 DE AC R14961.
 DE DT 02-FEB-1996 (first entry)
 DE DE Anti-Idiotypic antibody Idiotypic clone 17CB7.
 DE NM Antibody; cancer; anti-Idiotypic; CDR: heavy chain; light chain;

PR 24-JUN-1987: US-075578.
 PR 11-JAN-1988: US-440239.
 PR 08-DEC-1992: US-587555.
 PR 28-AUG-1994: US-589085.
 PR 11-JUN-1988: US-075288.
 PR (XOMA) XOMA CORP.
 PI Better M. Horvitz AH, Lei S, Liu AY, Robinson RR.
 PI Wall R, Wilcox GL.
 PI N-PSDB 003197/03.
 PT Production of chimeric antibody fragments - by culturing E. coli
 PT transformed with diastrophic expression cassette.
 CC The present invention was used in the development of a novel method
 CC for the production of a monoclonal antibody (Ig) fragment capable of
 CC binding an antigen. The method comprises culturing a host cell
 CC that has been transformed with a nucleic acid molecule encoding the
 CC Ig fragment, under conditions so that the Ig fragment is produced
 CC and secreted. (a) pericatalase secretion signal sequence
 CC encoding a DNA sequence encoding at least the variable
 CC region of the Ig molecule; and (b) pericatalase secretion signal sequence
 CC region of the Ig molecule encoding at least the variable
 CC region of the Ig molecule. The method is used to produce chimeric Fab
 CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
 CC to a single proteolytic promoter to produce chimeric Fab
 CC molecules. The invention provides a novel approach for the production of
 CC recombinant antibody fragments and recombinant antibodies of
 CC expression in genetically engineered organisms. The application of
 CC specific Ig chains in vivo, recombinant DNA cloning and production of
 CC solution for the efficient large scale production of effective
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.
 CC Sequence 140 AA.
 DE Query Match 12.44; Score 19; DB 29; Length 140;
 DE Best Local Similarity 100.0%; Pred. No. 138e-11;
 DE Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 14 ttrphagatvvaakttpp 32
 DB 14 ttrphagatvvaakttpp 32
 DE RESULT 11
 DE ID M47520 standard; Protein: 140 AA.
 DE AC M47520;

DE Immunoglobulin: complementarily determining region.
 DE Mus sp.
 DE Key Location/Qualifiers
 DE Peptide 1-10
 DE 10701099-3
 DE 18-APR-1995
 DE 06-OCT-1993: JP-723950.
 DE 06-OCT-1993: JP-723950.
 DE WPI 02-180247/24.
 DE N-PSDB: 090436
 DE Novel anti-Idiotypic antibody against a human anticancer monoclonal
 DE antibody, and DNA sequence encoding the antibody, useful in
 DE treatment of cancer. The antibody is a heavy chain variable region
 DE Example 5: Page 14: 58pp; English.
 DE CC R14960-R14969 are clones of the anti-Idiotypic monoclonal antibody
 CC R14960, Idiotypic and Idiotypic against a human anticancer monoclonal antibody.
 CC medical uses and DNA encoding them are useful in pharmacological,
 CC and pharmaceutical fields of research.
 CC Sequence 135 AA.
 DE Query Match 12.44; Score 19; DB 14; Length 135;
 DE Best Local Similarity 100.0%; Pred. No. 138e-11;
 DE Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE 116 ldygagatvvaakttpp 134
 DE 134 ldygagatvvaakttpp 142
 DE RESULT 10
 DE ID M41070 standard; Protein: 140 AA.
 DE AC M41070.
 DE DT 01-JUN-1998 (first entry)
 DE DE Mouse 2H7 antibody heavy chain variable region.
 DE NM Immunoglobulin heavy chain; variable region.
 DE Monoclonal antibody 2H7; human B-cell surface antigen.
 DE Mus sp.
 DE Key Location/Qualifiers
 DE Peptide 1-19
 DE 05660103-A
 DE 02-DEC-1997
 DE 25-MAY-1995: 450731.
 DE 25-MAY-1995: US-501092.
 DE 01-NOV-1985: US-793980.
 DE 27-OCT-1985: WO-002285.

DE 05-JUN-1998 (first entry)
 DE Mouse 2H7 antibody heavy chain variable region.
 DE NM Immunoglobulin heavy chain; variable region.
 DE Monoclonal antibody 2H7; human B-cell surface antigen.
 DE Mus sp.
 DE Key Location/Qualifiers
 DE Peptide 1-19
 DE 05668417-A
 DE 02-DEC-1997
 DE 25-MAY-1995: 465203
 DE 25-MAY-1995: US-501092.
 DE 01-NOV-1985: US-793980.
 DE 27-OCT-1985: WO-002285.
 DE 11-JUN-1988: US-075288.
 DE 08-DEC-1992: US-587555.
 DE 18-AUG-1994: US-589085.
 DE 25-MAY-1995: US-450731.
 DE 25-MAY-1995: US-501092.
 DE (XOMA) XOMA CORP.
 PI Better M. Horvitz AH, Lei S, Liu AY, Robinson RR.
 PI Wall R, Wilcox GL.
 PI N-PSDB 003197/03.
 PT Production of recombinant immunoglobulin fragment - comprising Pd
 PT molecule and light chain. English.
 CC The present invention was used in the development of a novel method
 CC for the production of a monoclonal antibody (Ig) fragment capable of
 CC binding an antigen. The method comprises culturing a host cell
 CC that has been transformed with a nucleic acid molecule encoding the
 CC Ig fragment, under conditions so that the Ig fragment is produced
 CC and secreted. (a) pericatalase secretion signal sequence
 CC encoding a DNA sequence encoding at least the variable
 CC region of the Ig molecule; and (b) pericatalase secretion signal sequence
 CC region of the Ig molecule encoding at least the variable
 CC region of the Ig molecule. The method is used to produce chimeric Fab
 CC molecules, e.g. derived from murine monoclonal antibody 2H7 raised
 CC to a single proteolytic promoter to produce chimeric Fab
 CC molecules. The invention provides a novel approach for the production of
 CC recombinant antibody fragments and recombinant antibodies of
 CC expression in genetically engineered organisms. The application of
 CC specific Ig chains in vivo, recombinant DNA cloning and production of
 CC solution for the efficient large scale production of effective
 CC monoclonal antibodies. The invention also provides a solution to
 CC the problem of class switching antibody molecules.
 CC Sequence 140 AA.

CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
CC Sequence 140 AA:
Query Match 12.44: Score 19: DB 29: Length 140:
Best Local Similarity 100.00: Pred. No. 138e-11:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 14 TITVHSDVYDQSSALVIR 32
QY 14 TITVHSDVYDQSSALVIR 32

RESULT 12
ID W47513 standard: Protein: 140 AA.
AC W47513.1998 (first entry)
DE Mouse 2H7 antibody heavy chain variable region.
KW Mouse; murine; heavy chain; variable region;
KW Immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody 2H7; human B-cell surface antigen.
KW heavy ap.
FT Key ap. Location/Qualifiers
FT Peptide 1-19
FT /label= sig.peptide
FT /label= mat.peptide
FT US5698435-A.
FT 16-DEC-1997.
FT 06-JUN-1995: 467140.
FT 01-JAN-1997: 467140.
FT 01-JAN-1997: 467140.
FT 27-OCT-1986: WO-002289.
FT 27-OCT-1986: WO-002289.
FT 24-JUL-1987: US-077528.
FT 11-JAN-1988: US-142039.
FT 01-DEC-1987: US-077528.
FT 18-AUG-1994: US-390053.
FT 06-JUN-1995: US-467140.
FT (XOMA) XOMA CORP.
FT Better M. Horvitz AB, Lei S, Liu AY, Robinson RR,
FT Wall R, Wilcox CL.
FT WPI: 98-051492/05.
FT N-PSDB: V18557.
PT DNA encoding secreted immunoglobulin fragments - comprising at
PT least one variable region of light or heavy chains
PT Heavy chain, variable region of light or heavy chains
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (19) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host

FT /label= FR2
FT /note= "framework region 2"
FT region
FT 69..85
FT /label= CDR2
FT /note= "complementarily determining region 2"
FT region
FT 90..117
FT /label= FR3
FT /note= "framework region 3"
FT region
FT 118..130
FT /label= CDR3
FT /note= "complementarily determining region 3"
FT region
FT 131..140
FT /label= FR4
FT /note= "framework region 4"
FT US5698435-A.
FT 16-DEC-1997.
FT 06-JUN-1995: 467140.
FT 01-JAN-1997: 467140.
FT 01-JAN-1997: 467140.
FT 27-OCT-1986: WO-002289.
FT 27-OCT-1986: WO-002289.
FT 24-JUL-1987: US-077528.
FT 11-JAN-1988: US-142039.
FT 01-DEC-1987: US-077528.
FT 18-AUG-1994: US-390053.
FT 06-JUN-1995: US-467140.
FT (XOMA) XOMA CORP.
FT Better M. Horvitz AB, Lei S, Liu AY, Robinson RR,
FT Wall R, Wilcox CL.
FT WPI: 97-225493/20.
FT N-PSDB: V18557.
PT DNA encoding secreted immunoglobulin heavy and light chain fragments - capable
PT of assembling into chimeric antibodies, useful for e.g. passive
PT immunization, diagnosis, etc.
PT Example 4: Fig 21: 98pp: English.
PT A 2H7 antibody heavy chain variable region of
PT mouse monoclonal antibody 2H7 which recognizes human B-cell
PT antigen B220. It is encoded by a cDNA clone (T70868) obtained from a
PT 2H7 cDNA library by PCR amplification. The 2H7 light chain variable
PT sequence (W47514) is also provided. A novel human-mouse chimeric
PT antibody is constructed specifically for the human B-cell antigen has been
PT constructed.
SO Sequence 140 AA:
Query Match 12.44: Score 19: DB 29: Length 140:
Best Local Similarity 100.00: Pred. No. 138e-11:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

CC this has been transformed with a nucleic acid molecule encoding the
CC heavy chain variable region of a human antibody, the heavy chain
CC and secreted. The nucleic acid molecule comprises DNA sequences
CC encoding: (a) peptide lyase secretion signal sequence operably
CC linked to a DNA sequence encoding at least the variable region of
CC antibody, and (b) peptide lyase secretion signal sequence
CC operably linked to a DNA sequence encoding at least the variable
CC region of an Ig light chain, where (a) and (b) are operably linked
CC to a single prokaryotic promoter to form a dicistronic
CC transcription unit. The method is used to produce chimeric Fab
CC antibodies. The antibodies are used for immunodiagnosis, raised
CC against human B-cell surface antigen B220. The invention provides a
CC novel approach for producing genetically engineered antibodies of
CC desired variable region specificity and constant region
CC properties. The cloned Ig gene products can be produced by
CC chemical gene synthesis, recombinant DNA cloning and production of
CC specific Ig chains in various organisms provides an effective
CC solution for the efficient large scale production of human
CC monoclonal antibodies. The invention also provides a solution to
CC the problem of class switching antibody molecules.
CC Sequence 140 AA:
Query Match 12.44: Score 19: DB 29: Length 140:
Best Local Similarity 100.00: Pred. No. 138e-11:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 14 TITVHSDVYDQSSALVIR 32
QY 14 TITVHSDVYDQSSALVIR 32

RESULT 12
ID W47513 standard: Protein: 140 AA.
AC W47513.1998 (first entry)
DE Mouse 2H7 antibody heavy chain variable region.
KW Mouse; murine; heavy chain; variable region;
KW Immunoglobulin fragment production; Ig fragment production;
KW monoclonal antibody 2H7; human B-cell surface antigen.
KW heavy ap.
FT Key ap. Location/Qualifiers
FT Peptide 1-19
FT /label= sig.peptide
FT /label= mat.peptide
FT US5698435-A.
FT 16-DEC-1997.
FT 06-JUN-1995: 467140.
FT 01-JAN-1997: 467140.
FT 01-JAN-1997: 467140.
FT 27-OCT-1986: WO-002289.
FT 27-OCT-1986: WO-002289.
FT 24-JUL-1987: US-077528.
FT 11-JAN-1988: US-142039.
FT 01-DEC-1987: US-077528.
FT 18-AUG-1994: US-390053.
FT 06-JUN-1995: US-467140.
FT (XOMA) XOMA CORP.
FT Better M. Horvitz AB, Lei S, Liu AY, Robinson RR,
FT Wall R, Wilcox CL.
FT WPI: 98-051492/05.
FT N-PSDB: V18557.
PT DNA encoding secreted immunoglobulin fragments - comprising at
PT least one variable region of light or heavy chains
PT Heavy chain, variable region of light or heavy chains
CC The present sequence was used in the development of a novel method
CC for the production of an immunoglobulin (19) fragment capable of
CC binding an antigen. The method comprises culturing an E. coli host

FT /label= FR2
FT /note= "framework region 2"
FT region
FT 69..85
FT /label= CDR2
FT /note= "complementarily determining region 2"
FT region
FT 90..117
FT /label= FR3
FT /note= "framework region 3"
FT region
FT 118..130
FT /label= CDR3
FT /note= "complementarily determining region 3"
FT region
FT 131..140
FT /label= FR4
FT /note= "framework region 4"
FT US5698435-A.
FT 16-DEC-1997.
FT 06-JUN-1995: 467140.
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FT 27-OCT-1986: WO-002289.
FT 27-OCT-1986: WO-002289.
FT 24-JUL-1987: US-077528.
FT 11-JAN-1988: US-142039.
FT 01-DEC-1987: US-077528.
FT 18-AUG-1994: US-390053.
FT 06-JUN-1995: US-467140.
FT (XOMA) XOMA CORP.
FT Better M. Horvitz AB, Lei S, Liu AY, Robinson RR,
FT Wall R, Wilcox CL.
FT WPI: 97-225493/20.
FT N-PSDB: V18557.
PT DNA encoding secreted immunoglobulin heavy and light chain fragments - capable
PT of assembling into chimeric antibodies, useful for e.g. passive
PT immunization, diagnosis, etc.
PT Example 4: Fig 21: 98pp: English.
PT A 2H7 antibody heavy chain variable region of
PT mouse monoclonal antibody 2H7 which recognizes human B-cell
PT antigen B220. It is encoded by a cDNA clone (T70868) obtained from a
PT 2H7 cDNA library by PCR amplification. The 2H7 light chain variable
PT sequence (W47514) is also provided. A novel human-mouse chimeric
PT antibody is constructed specifically for the human B-cell antigen has been
PT constructed.
SO Sequence 140 AA:
Query Match 12.44: Score 19: DB 29: Length 140:
Best Local Similarity 100.00: Pred. No. 138e-11:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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FT	misc_difference	108
FT	misc_difference	/note="mutation v.r.t. original sequence"
FT	W0311633.1	
PR	21-NR-1991	E00761
PR	23-APR-1990	EP-401090.
PR	(CORV.) CORVAS INT NV.	
PR	LaRoche J, Moloney P, Demaezner M;	
PT	New single-chain VhAs specific to asp. fibrin - used for imaging,	
PT	and when connected to plasmidogen activating portion used for	
PT	lysis of thrombi.	
CC	A239-8233 may be similar to 5c, 18pp2 English	
CC	imaging of thrombi. The scA may be labelled and used for the	
CC	imaging of thrombi. The scA may be connected, via a 2nd linker	
CC	(lead) to a plasmidogen activating portion (PA-portion), pref. a	
CC	thymidine domain of E19 or uridine, esp. acsu), to form a	
CC	and has a lower mol. wt. than similar genes and an increased half-life	
CC	expected to have a reduced immunogenicity and improved thrombolytic	
CC	specificity.	
CC	Sequence Q1467-70 and R14694-703 and R15690-93.	
CC	Sequence Q135-AM.	
CC	Sequence Q135-AM.	
Q	Query Match	112.4%; Score 19; DB 3; Length 235;
Q	Local Similarity	100.0%; Pred No. 1,384-11;
M	Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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D	125	dwmoosvpsvpsanattpp 143
D	125	dwmoosvpsvpsanattpp 143
RESULT	30	standard; Protein: 236 AA.
AC	R15690	
DT	01-FEB-1993	(first entry)
DE	1-F1b-Vh construction (44), single chain antibody.	
OS	CA; SDAH; Trombas; F-P; urokinase.	
OS	SwissProt	
FT	key	Location/Qualifiers
FT	region	1..108
FT	region	/label=Vh

OS	Synthetic.
FR	Key
FR	region
FR	1..108
FR	/label= V1
FR	region
FR	109..117
FR	/label= Lab
FR	region
FR	118..237
FR	/label= Vb
FR	region
FR	109..104
FR	/label= V1_anchor_region
FR	120..124
FR	/label= Vb_anchor_region
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FR	misc_difference 108
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FR	/note= "mutation v.r.t. original sequence"
PN	NO9161635.N.
PN	31-06-1981
PD	21-08-1981
PR	21-08-1981
PA	(CORV.) CORVAS INT W.
PI	Larchoe Y, Holwegt P, Demayer M:
PN	WPI: 91-335/63/46
PT	and when connected to plasmidogen activating portion used for
PT	lysis of thrombi
CC	Disclosure: P4g 6; 78pp; English.
CC	A231-537 may be omitted. The SCN can be labelled and used for the
CC	labeling of fibrin. The SCN may be connected, via a 2nd linker
CC	catalytic domain of tPA or urokinase, to a specific, e.g. a
CC	thrombolytic agent (SCoPA). The SCoPA has an increased half-life
CC	and has a lower mol. wt. than similar agents and is therefore
CC	expected to have a reduced immunogenicity and improved thrombus
CC	See also 01448-70 and R1469-70 and R1560-93.
CC	Sequence 337 Aa.

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FT      region
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FT      /label= Vh_anchor_region
FT      119..123
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FT      21-DEC-1991. E00767
FT      21-APR-1990. EP-401090.
FT      (CONV.) CORVAS INT NV.
FT      Laroche Y, Holvoet P, Demeyer M.
FT      New antigen 159/63/46
FT      highly specific to epd, fibrin - used for imaging,
FT      and when connected to plasmidogen activating portion used for
FT      lysis of thrombi
FT      /note= "Fig 6, 7bpg, English.
FT      Discharge"
FT      The SCA can be labeled and used for the
FT      imaging of thrombi and the SCA may be
FT      (lead) to a plasmidogen activating portion (PA-portion) and linker
FT      catalytic domain of t-PA or urokinase, esp. scup, to form a
FT      enzymolytic agent (SCA-PA). The SCA-PA has an increased half-life
FT      expected to have a reduced immunogenicity and is therefore
FT      penetration.
FT      See also Q14468-70 and R14594-703 and R15690-93.
FT      sequence 216 MA.
FT
FT      Query March
FT      Best Local Similarity 100.00; Pcd. No. 138-111;
FT      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps
FT
FT      Db 217 dyggsgtvtvssatrtpp 235
FT      |||||||
FT      Oy 123 DYWGCGTSTVSSATRTTP 143
FT
FT      RESULT 31
FT      ID R15691 standard; Protein: 217 MA.
FT      DT 01-FEB-1992 (first entry)
FT      DT 01-FEB-1992 (first entry)
FT      DI Lab-Vh construction (44), single chain antibody.
FT      SCN, SCA-PA; trombus; t-PA; urokinase.
FT
FT      Key
FT      region
FT      /label= Vh
FT      Location/QuasiStere
FT      /label= Vh
FT      /note= "from MA-15C5"
FT      109..116
FT      /label= Lab
FT      119..123
FT      /label= Vh
FT      /note= "from MA-15C5"
FT      100..104
FT      /label= Vh_anchor_region
FT      121..125
FT      /label= Vh_anchor_region
FT      misc_difference 106
FT      /note= "mutation v.r.t. original sequence"
FT      /note= "mutation v.r.t. original sequence"
FT      W09116353-A.
FT      21-APR-1991. E00767
FT      21-APR-1990. EP-401090.
FT      (CONV.) CORVAS INT NV.
FT      Laroche Y, Holvoet P, Demeyer M.
FT      New antigen 159/63/46
FT      highly specific to epd, fibrin - used for imaging,
FT      and when connected to plasmidogen activating portion used for
FT      lysis of thrombi
FT      /note= "Fig 6, 7bpg, English.
FT      Discharge"
FT      The SCA can be labeled and used for the
FT      imaging of thrombi. The SCA may be
FT      (lead) to a plasmidogen activating portion (PA-portion), pref. a
FT      enzymolytic agent (SCA-PA). The SCA-PA has an increased half-life
FT      expected to have a reduced immunogenicity and is therefore
FT      penetration.
FT      See also Q14468-70 and R14594-703 and R15690-93.
FT      sequence 216 MA.
FT
FT      Query March
FT      Best Local Similarity 100.00; Pcd. No. 138-111;
FT      Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT      215 dyggsgtvtvssatrtpp 237
FT      |||||||
FT      123 DYWGCGTSTVSSATRTTP 143

```

RESULT 33
ID R16593 standard: Protein: 239 AA.
DE 01-FEB-1992 (first entry)
DE V1-Lab-VH construction (4A), single chain antibody.
KW SCA: SCAPA, trombus: t-PA, urokinase.
OS Synthetic.
FT region
FT 108
FT /label=V1
FT /note="from MA-15C5"
FT region
FT 109..119
FT /label=VH
FT /note="from MA-15C5"
FT region
FT 120..239
FT /label=VH
FT /note="from MA-15C5"
FT region
FT 121..126
FT /label=VH_anchor_region
FT /note="from MA-15C5"
FT misc_difference 108
FT /note="mutation v.r.t. original sequence"
FT misc_difference 108
FT /note="mutation v.r.t. original sequence"
FT W0116353.N.
FT 21-DEC-1991
FT 21-DEC-1991
FT 23-APR-1990: EP-401090.
PA (CORV-) CORVAS INT NW.
PI Laroche Y, Holvoet P, Demaeyer M;
PM 91-135763/46, the specific to cap. fibrin - used for imaging,
PT and when connected to plasminogen activating portion used for
PT lysate of thrombi.
PS Disclosure: Fig 6; 78pp: English.
CC 421-5833 may be omitted. The SCA can be labelled and used for the
CC imaging of thrombi. The SCA may be connected to the 2nd fibrin
CC (Lcd) to a plasminogen activating portion (PA-portion), pref. a
CC catalytic domain of t-PA or urokinase, esp. scupA, to form a
CC thrombolytic agent (SCAPA). The SCAPA has an increased half-life
CC expected to have a reduced immunogenicity and improved thrombus
CC penetration.
CC See also Q14466-70 and R14694-703 and R15690-93.
SQ Sequence 239 AA:
Query Match 12.4% Score 19: DB 3: Length 239;
Best Local Similarity 100.0%; Pred. No. 1.38e-11;
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RESULT 35
ID R76085 standard: Peptide: 445 AA.
DE 02-SEP-1986 (first entry)
DE MAD 55.1 heavy chain.
KW Antigen binding structure: complementarily determining region: CDR:
KW C455.1: colorectal cancer: tumor-associated antigen: hybridoma:
KW monoclonal antibody: MAb: immunotherapy: therapy: diagnosis:
KW humanized antibody: immunotoxin.
OS Mus sp.
PN M0515382.N.
PN 28-NOV-1994
PN 03-DEC-1993: DB-024619.
PR 03-JUN-1994: DB-011089.
PA (28NE) GENEXA LTD.
PI Rose NS, Wright AF;
PM 95-215262/28.
PT Antigen binding structures containing CDRs recognizing the C455.1
PT antigen, produced by hybridoma and host cells, for use in the
PT treatment of colorectal cancer. English.
PS Chain 3: Page 9799-121pp: English.
CC An antigen binding structure is based on the CDRs (given in R76078-
CC 84) of the heavy (R76085) and light (R76086) chains of MAb 55.1
CC (R76085/86). This structure is a monoclonal antibody (MAb) that
CC (F(ab')₂) Fab, Fv, scFv or V-chain, and is produced in transgenic
CC animals or plants.
SQ Sequence 445 AA:
Query Match 12.4% Score 19: DB 13: Length 445;
Best Local Similarity 100.0%; Pred. No. 1.38e-11;
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RESULT 36
ID R39643 standard: Protein: 448 AA.
AC R39643:
DE 11-OCT-1996 (first entry)
DE Anti-bovine growth hormone heavy chain.
KW Antibody engineering: single polypeptide chain binding molecule:
KW heavy chain: light chain: monoclonal antibody: MAb:
KW bovine growth hormone: bGH: immunoreactivity purification.

DB 220 dymggrtvtysakttpp 238
QY 125 dymggrtvtysakttpp 143
RESULT 34
ID R14698 standard: Protein: 243 AA.
DE 01-FEB-1992 (first entry)
DE V1-Lab-VH construction (4A), single chain antibody.
KW SCA: SCAPA, trombus: t-PA, urokinase.
OS Synthetic.
FT region
FT 108
FT /label=V1
FT /note="from MA-15C5"
FT region
FT 109..119
FT /label=VH
FT /note="from MA-15C5"
FT region
FT 120..243
FT /label=VH
FT /note="from MA-15C5"
FT region
FT 121..126
FT /label=VH_anchor_region
FT /note="from MA-15C5"
FT misc_difference 108
FT /note="mutation v.r.t. original sequence"
FT misc_difference 108
FT /note="mutation v.r.t. original sequence"
FT W0116353.N.
FT 21-DEC-1991
FT 21-DEC-1991
FT 23-APR-1990: EP-401090.
PA (CORV-) CORVAS INT NW.
PI Laroche Y, Holvoet P, Demaeyer M;
PM 91-135763/46, the specific to cap. fibrin - used for imaging,
PT and when connected to plasminogen activating portion used for
PT lysate of thrombi.
PS Disclosure: Fig 6; 78pp: English.
CC 421-5833 may be omitted. The SCA can be labelled and used for the
CC imaging of thrombi. The SCA may be connected to the 2nd fibrin
CC (Lcd) to a plasminogen activating portion (PA-portion), pref. a
CC catalytic domain of t-PA or urokinase, esp. scupA, to form a
CC thrombolytic agent (SCAPA). The SCAPA has an increased half-life
CC expected to have a reduced immunogenicity and improved thrombus
CC penetration.
CC See also Q14466-70 and R14694-703 and R15690-93.
SQ Sequence 243 AA:
Query Match 12.4% Score 19: DB 3: Length 243;
Best Local Similarity 100.0%; Pred. No. 1.38e-11;
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OS Mus sp.
PN M0515382.N.
PN 28-NOV-1994
PN 03-DEC-1993: DB-024619.
PR 03-JUN-1994: DB-011089.
PA (28NE) GENEXA LTD.
PI Rose NS, Wright AF;
PM 95-215262/28.
PT Antigen binding structures containing CDRs recognizing the C455.1
PT antigen, produced by hybridoma and host cells, for use in the
PT treatment of colorectal cancer. English.
PS Chain 3: Page 9799-121pp: English.
CC An antigen binding structure is based on the CDRs (given in R76078-
CC 84) of the heavy (R76085) and light (R76086) chains of MAb 55.1
CC (R76085/86). This structure is a monoclonal antibody (MAb) that
CC (F(ab')₂) Fab, Fv, scFv or V-chain, and is produced in transgenic
CC animals or plants.
SQ Sequence 448 AA:
Query Match 12.4% Score 19: DB 18: Length 448;
Best Local Similarity 100.0%; Pred. No. 1.38e-11;
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RESULT 37
ID R43673 standard: Protein: 448 AA.
AC R43673:
DE 23-NOV-1994 (first entry)
DE Mouse anti-bovine growth hormone MAb heavy chain.
KW Monoclonal antibody: MAb: affinity: binding: antigen: diagnostics:
KW therapy: imaging: purification: biosensors.
PN 05-NOV-1993
PN 09-NOV-1993
PF 02-SEP-1986: 902971.

!!SEQUENCE LIST 1.0
(Peptide) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-4 check: 265 from: 1

FROM: of: /home/obryen/ree455/olig/US08836455.pep
sequence 4, application us/08836455

general information:
applicant: chatterjee, malaya
applicant: toon, kenneth a.
applicant: chatterjee, sunil k. . .

TO: pir: * Sequences: 116,738 Total-length: 37,460,341 April 18, 1999 19:16

Database Release Information:

NRFR, Release 58.0, Released on 30Sep1998, Formatted on 15Dec1998

Word-size: 5 Words: 56967 Diagonals: 6,675 Total-diagonals: 55,204,517
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 4.59

Sequence Strd Diag Score Width Documentation ..

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PIR2:S42177	+	-26	73	1	Ig gamma chain V region - mouse (frag
PIR2:S42181	+	-26	73	1	Ig gamma chain V region - mouse (frag
PIR2:S42176	+	-26	73	1	Ig gamma chain V region - mouse (frag
PIR2:S42184	+	-19	73	1	Ig gamma chain V region - mouse (frag
PIR2:S42179	+	-19	73	1	Ig gamma chain V region - mouse (frag
PIR2:S42180	+	-19	73	1	Ig gamma chain V region - mouse (frag
PIR2:S25057	+	0	69	1	Ig gamma-2b chain - mouse
PIR2:H32513	+	0	68	1	Ig heavy chain precursor V region (B)
PIR2:PH1000	+	-19	67	1	Ig heavy chain V region (clone 202.10
PIR2:S41394	+	-19	67	1	Ig heavy chain V region - mouse
PIR1:HVM502	+	0	66	1	Ig heavy chain precursor V region (10
PIR2:S37201	+	-19	65	1	Ig heavy chain V region - mouse
PIR1:HVM507	+	0	64	1	Ig heavy chain precursor V region (9)
PIR2:PH1494	+	0	64	1	Ig heavy chain V region (clones X7-30
PIR2:PH1484	+	0	64	1	Ig heavy chain V region (clones X7-30
PIR2:PH1482	+	0	64	1	Ig heavy chain V region (clones 36-35
PIR2:S38717	+	-19	64	1	Ig heavy chain V region - mouse
PIR2:PH1486	+	0	63	1	Ig heavy chain V region (clone X7-30)
PIR2:A27609	+	0	63	1	Ig heavy chain precursor V region (12
PIR2:PI10247	+	-22	63	1	Ig heavy chain V region (anti-DNA, 11
PIR2:A39276	+	0	63	1	Ig heavy chain precursor V-D-J region
PIR2:S21810	+	-13	62	1	Ig heavy chain V region (clone X7-5D3
PIR2:PH1512	+	0	62	1	Ig heavy chain V region (clone X7-4G7
PIR2:PH1498	+	-19	62	1	Ig heavy chain V region (clone 111.66
PIR2:S20643	+	-19	62	1	Ig heavy chain V region - mouse
PIR2:A54378	+	0	61	1	Ig heavy chain V region anti-triplex
PIR1:HVM58A	+	0	61	1	Ig heavy chain precursor V region (10
PIR2:PS0024	+	-19	61	1	Ig heavy chain precursor V region (6)
PIR2:PH1005	+	-19	61	1	Ig heavy chain V region (clone 202.54
PIR2:S38950	+	-19	61	2	Ig gamma chain - mouse
PIR2:S40295	+	-19	61	2	Ig gamma-2a chain (mb735) - mouse
PIR2:S53751	+	-19	61	1	antibody Fab Jcl 103 heavy chain - mc
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PIR2:PH1493	+	0	59	1	Ig heavy chain V region (clone PR14-3
PIR2:PH0998	+	-19	59	1	Ig heavy chain V region (clone 165.3)
PIR2:PH1492	+	0	59	1	Ig heavy chain V region (clone PR11-4
PIR2:S01321	+	0	59	1	Ig gamma-2b chain precursor - mouse
PIR2:S55541	+	-20	59	1	Ig heavy chain V region (clone X7-5D3
PIR2:PH1500	+	-13	58	1	Ig heavy chain V region (clone X41-2)
PIR2:PH1489	+	0	58	1	Ig heavy chain V region (clones X7-57
PIR2:PH1504	+	-13	58	1	Ig heavy chain V region (clones X7-57
PIR2:PH1522	+	-13	58	1	Ig heavy chain V region (clone PR14-3
PIR2:PH1521	+	-13	58	1	Ig heavy chain V region (clone X41-32
PIR2:PH0989	+	-19	58	1	Ig heavy chain V region - mouse (frag
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not doing anything with the data as long

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MPSEARCH (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit,
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MPSEARCH protein - protein database search, using Smith-Waterman algorithm
Run on: Thu Apr 15 18:11:03 1999; MaxFit time 8.10 Seconds
Tabular output not generated.

File: >US-08-836-455-4
Description: (7515) from 0808063455.psp
Percent Score: 1 MEGSWFPLM17CVHSO.....TWSSAKTPPPVPLVPGSL 153
Sequence: 1 MEGSWFPLM17CVHSO.....TWSSAKTPPPVPLVPGSL 153

Scoring table: TBLASTX uniprotcable
Gap 60

Searched: 116695 seqs, 37453910 residues
Post-processing: Minimum Match 08
Listing first 1000 summaries

Database: P1598 1:PIR1 2:PIR2 3:PIR3 4:PIR4
Statistics: Mean 3.358; Variance 0.508; scale 6.516

Pred. No. is the number of results predicted by chance to have a
score at least as high as the observed score. The score is printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Entry Match	Length	DB	ID	Description	Pred. No.
1	22	14.4	119	2	PI0089	19 heavy chain V regl	6.58e-33

104	14	9.2	118	2	PI0011	19 heavy chain precut	6.58e-33
103	14	9.2	118	2	PI0012	19 gamma chain V regl	4.94e-28
102	14	9.2	118	2	PI0013	19 gamma chain V regl	4.94e-28
101	14	9.2	118	2	PI0014	19 gamma chain V regl	4.94e-28
100	14	9.2	118	2	PI0015	19 gamma chain V regl	4.94e-28
99	14	9.2	118	2	PI0016	19 gamma chain V regl	4.94e-28
98	14	9.2	118	2	PI0017	19 gamma chain V regl	4.94e-28
97	14	9.2	118	2	PI0018	19 gamma chain V regl	4.94e-28
96	14	9.2	118	2	PI0019	19 gamma chain V regl	4.94e-28
95	14	9.2	118	2	PI0020	19 gamma chain V regl	4.94e-28
94	14	9.2	118	2	PI0021	19 gamma chain V regl	4.94e-28
93	14	9.2	118	2	PI0022	19 gamma chain V regl	4.94e-28
92	14	9.2	118	2	PI0023	19 gamma chain V regl	4.94e-28
91	14	9.2	118	2	PI0024	19 gamma chain V regl	4.94e-28
90	14	9.2	118	2	PI0025	19 gamma chain V regl	4.94e-28
89	14	9.2	118	2	PI0026	19 gamma chain V regl	4.94e-28
88	14	9.2	118	2	PI0027	19 gamma chain V regl	4.94e-28
87	14	9.2	118	2	PI0028	19 gamma chain V regl	4.94e-28
86	14	9.2	118	2	PI0029	19 gamma chain V regl	4.94e-28
85	14	9.2	118	2	PI0030	19 gamma chain V regl	4.94e-28
84	14	9.2	118	2	PI0031	19 gamma chain V regl	4.94e-28
83	14	9.2	118	2	PI0032	19 gamma chain V regl	4.94e-28
82	14	9.2	118	2	PI0033	19 gamma chain V regl	4.94e-28
81	14	9.2	118	2	PI0034	19 gamma chain V regl	4.94e-28
80	14	9.2	118	2	PI0035	19 gamma chain V regl	4.94e-28
79	14	9.2	118	2	PI0036	19 gamma chain V regl	4.94e-28
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75	14	9.2	118	2	PI0040	19 gamma chain V regl	4.94e-28
74	14	9.2	118	2	PI0041	19 gamma chain V regl	4.94e-28
73	14	9.2	118	2	PI0042	19 gamma chain V regl	4.94e-28
72	14	9.2	118	2	PI0043	19 gamma chain V regl	4.94e-28
71	14	9.2	118	2	PI0044	19 gamma chain V regl	4.94e-28
70	14	9.2	118	2	PI0045	19 gamma chain V regl	4.94e-28
69	14	9.2	118	2	PI0046	19 gamma chain V regl	4.94e-28
68	14	9.2	118	2	PI0047	19 gamma chain V regl	4.94e-28
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65	14	9.2	118	2	PI0050	19 gamma chain V regl	4.94e-28
64	14	9.2	118	2	PI0051	19 gamma chain V regl	4.94e-28
63	14	9.2	118	2	PI0052	19 gamma chain V regl	4.94e-28
62	14	9.2	118	2	PI0053	19 gamma chain V regl	4.94e-28
61	14	9.2	118	2	PI0054	19 gamma chain V regl	4.94e-28
60	14	9.2	118	2	PI0055	19 gamma chain V regl	4.94e-28
59	14	9.2	118	2	PI0056	19 gamma chain V regl	4.94e-28
58	14	9.2	118	2	PI0057	19 gamma chain V regl	4.94e-28
57	14	9.2	118	2	PI0058	19 gamma chain V regl	4.94e-28
56	14	9.2	118	2	PI0059	19 gamma chain V regl	4.94e-28
55	14	9.2	118	2	PI0060	19 gamma chain V regl	4.94e-28
54	14	9.2	118	2	PI0061	19 gamma chain V regl	4.94e-28
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Best Local Similarity 100.0%: Pred. No. 4,94e-28:
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 23 TSYNNHWKOTPOGCLNIG 42
QY 49 TSYNNHWKOTPOGCLNIG 68

RESULT 6
ENTRY 542181 *type fragment
TITLE Ig gamma chain V region - mouse (fragment)
ORIGIN 19 gamma chain V region - mouse (fragment)
DATE 26-Sep-1994 sequence_revision 21-Jul-1995 text_change
FEATURES
ACCESSIONS 542181
AUTHORS No, J. A.; Bone, C. A.; Holmstedt, R.
JOURNAL Immunol. (1993) 23:2503-2510
REFERENCE Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
*accession 542181 preliminary
**residues 1-97 **label MOJ
**cross-reference EMBL:Z25451; NID:9407820; PID:9407821
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
FEATURES
SDMMARY 8-91 *domain Immunoglobulin homology #label IMM
length 97 *checksum 1319
Query Match      13.1% Score 20: DB 2: Length 97:
Best Local Similarity 100.0%: Pred. No. 4,94e-28:
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 23 TSYNNHWKOTPOGCLNIG 42
QY 49 TSYNNHWKOTPOGCLNIG 68

RESULT 7
ENTRY 542179 *type fragment
TITLE Ig gamma chain V region - mouse (fragment)
ORIGIN 19 gamma chain V region - mouse (fragment)
DATE 26-Sep-1994 sequence_revision 21-Jul-1995 text_change
FEATURES
ACCESSIONS 542179
AUTHORS No, J. A.; Bone, C. A.; Holmstedt, R.
JOURNAL Immunol. (1993) 23:2503-2510
REFERENCE Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
*accession 542179 preliminary
**residues 1-97 **label MOJ
**cross-reference EMBL:Z25451; NID:9407820; PID:9407821
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
FEATURES
SDMMARY 8-91 *domain Immunoglobulin homology #label IMM
length 97 *checksum 1319
Query Match      13.1% Score 20: DB 2: Length 97:
Best Local Similarity 100.0%: Pred. No. 4,94e-28:
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 23 TSYNNHWKOTPOGCLNIG 42
QY 49 TSYNNHWKOTPOGCLNIG 68

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Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 30 TSYNNHWKOTPOGCLNIG 49
QY 49 TSYNNHWKOTPOGCLNIG 68

RESULT 9
ENTRY 542180 *type fragment
TITLE Ig gamma chain V region - mouse (fragment)
ORIGIN 19 gamma chain V region - mouse (fragment)
DATE 26-Sep-1994 sequence_revision 21-Jul-1995 text_change
FEATURES
ACCESSIONS 542180
AUTHORS No, J. A.; Bone, C. A.; Holmstedt, R.
JOURNAL Immunol. (1993) 23:2503-2510
REFERENCE Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
*accession 542180 preliminary
**residues 1-102 **label MOJ
**cross-reference EMBL:Z25449; NID:9407818; PID:9407819
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
FEATURES
SDMMARY 15-98 *domain Immunoglobulin homology #label IMM
length 102 *checksum 8407
Query Match      13.1% Score 20: DB 2: Length 101:
Best Local Similarity 100.0%: Pred. No. 4,94e-28:
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 30 TSYNNHWKOTPOGCLNIG 49
QY 49 TSYNNHWKOTPOGCLNIG 68

RESULT 10
ENTRY 514238 *type fragment
TITLE Ig gamma-1 chain precursor (LSCS) - mouse (fragment)
ORIGIN 19 gamma-1 chain precursor (LSCS) - mouse (fragment)
DATE 25-Feb-1994 sequence_revision 10-Nov-1995 text_change
FEATURES
ACCESSIONS 514238
AUTHORS Vadas, A. M.; Bulens, F.; Bernat, H.; Molles, L.; Lijnen,
R. R.; Collen, D.; Blochem, (1990) 193:767-775
*journal

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AUTHORS No, J. A.; Bone, C. A.; Holmstedt, R.
JOURNAL Immunol. (1993) 23:2503-2510
REFERENCE Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
*accession 542181 preliminary
**residues 1-101 **label MOJ
**cross-reference EMBL:Z25447; NID:9407816; PID:9407817
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
FEATURES
SDMMARY 15-98 *domain Immunoglobulin homology #label IMM
length 101 *checksum 4698
Query Match      13.1% Score 20: DB 2: Length 101:
Best Local Similarity 100.0%: Pred. No. 4,94e-28:
Matches 20: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 30 TSYNNHWKOTPOGCLNIG 49
QY 49 TSYNNHWKOTPOGCLNIG 68

RESULT 8
ENTRY 542184 *type fragment
TITLE Ig gamma chain V region - mouse (fragment)
ORIGIN 19 gamma chain V region - mouse (fragment)
DATE 26-Sep-1994 sequence_revision 21-Jul-1995 text_change
FEATURES
ACCESSIONS 542184
AUTHORS No, J. A.; Bone, C. A.; Holmstedt, R.
JOURNAL Immunol. (1993) 23:2503-2510
REFERENCE Variable region gene selection of immunoglobulin G-expressing
B cells with specificity for a defined epitope on type II
collagen.
*accession 542184 preliminary
**residues 1-101 **label MOJ
**cross-reference EMBL:Z25457; NID:951619; PID:9747823
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
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length 101 *checksum 5378
Query Match      13.1% Score 20: DB 2: Length 101:
Best Local Similarity 100.0%: Pred. No. 4,94e-28:

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TITLE Construction and characterization of a recombinant murine
antibody directed against human fibrin
*accession 514238
**residues 1-101 **label MOJ
**cross-reference EMBL:Z25457; NID:951619; PID:9747823
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
FEATURES
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length 101 *checksum 5378
Query Match      13.1% Score 19: DB 2: Length 140:
Best Local Similarity 100.0%: Pred. No. 1.12e-25:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 116 DPMQGGIVYVSANATTP 134
QY 125 DPMQGGIVYVSANATTP 143

RESULT 11
ENTRY 530752 *type complete
TITLE Ig gamma chain V region - mouse
ORIGIN 19 gamma chain V region - mouse
DATE 31-Dec-1993 sequence_revision 31-Dec-1993 text_change
FEATURES
ACCESSIONS 530752
AUTHORS Grant, F. J.; Leyva, S. D.; Gilbert, T.; Kindsvogel, W.
JOURNAL Nucleic Acids Res. (1987) 15:5495
REFERENCE Improved RNA sequencing method to determine immunoglobulin
variable region sequence.
*accession 530752
**residues 610752
**molecule-type mRNA
**cross-reference 1-149 **label GRB
**cross-reference EMBL:X0876; NID:953536; PID:953227
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
FEATURES
SDMMARY 13-116 *domain Immunoglobulin homology #label IMM
length 149 *molecular-weight 16635 *checksum 9814
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Best Local Similarity 100.0%: Pred. No. 1.32e-25:
Matches 19: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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DB 125 DYNOCGCTVTSANKTPP 143
OY 125 DYNOCGCTVTSANKTPP 143

RESULT 12
ENTRY P00444 #type fragment
TITLE Ig heavy chain V region precursor - human (fragment)
ORIGINISM 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
DATE 15-Aug-1998
ACCESSIONS P00444
REFERENCES Kallus, B.; Betel, G.; Shao, H.; Diamantstein, T.; Wiedle,
#journal gene (1992) 123:321-328
#title A general method for characterization of monoclonal antibodies
#abstract by inverse polymerase chain reaction which conserves
#accession P00444
#molecule_type mRNA
#residues 1-150 #label KAL
CLASSIFICATION #cross-reference G0:102316
REMARKS #superfamily Immunoglobulin V region: Immunoglobulin homology
FEATURES
1-130 #domain signal sequence #status predicted #label SIGV
20-130 #product Ig heavy chain V region #status predicted
#domain variable region #label VMC
20-117 #length 150 #checksum 9720

Query Match
Best Local Similarity 10.0 #score 19; DB 2; Length 150;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 125 DYNOCGCTVTSANKTPP 143
OY 125 DYNOCGCTVTSANKTPP 143

RESULT 13
ENTRY S26471 #type complete
TITLE Ig heavy chain V region (KAL3) - mouse
ORIGINISM 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change
DATE 07-Aug-1998
ACCESSIONS S26471
REFERENCES Buckel, P.; Hubner-Parajcs, C.; Mattea, R.; Lanz, H.; Nagy,
#journal R.; Beaucamp, R.
#abstract
#accession S26471
#molecule_type mRNA
#residues 1-178 #label SPY
CLASSIFICATION #cross-reference EMBL:X57857; NID:952591
REMARKS #superfamily Immunoglobulin V region: Immunoglobulin homology
FEATURES
1-178 #domain signal sequence #status predicted #label SIGV
05-Jun-1988 #product Ig heavy chain V region #status predicted
#domain variable region #label VMC
05-Jun-1988 #length 178 #checksum 9799

Query Match
Best Local Similarity 100.0 #score 19; DB 2; Length 178;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 119 DYNOCGCTVTSANKTPP 137
OY 125 DYNOCGCTVTSANKTPP 143

RESULT 15
ENTRY S06824 #type complete
TITLE Ig heavy chain V region (clone 12d4) - mouse
ORIGINISM 30-Sep-1991 #sequence_revision 11-Nov-1991 #text_change
DATE 08-Sep-1997
ACCESSIONS S06824
REFERENCES J. Mol. Biol. (1988) 209:763-778
#journal Comparative sequence and immunohistochemical analyses of murine
#abstract monoclonal anti-morphine antibodies.
#accession S06824
#molecule_type mRNA
#residues 1-124 #label MTL
CLASSIFICATION #cross-reference EMBL:X17166; NID:951918; PID:9310156
REMARKS #superfamily Immunoglobulin V region: Immunoglobulin homology
FEATURES
1-124 #domain signal sequence #status predicted #label SIGV
11-Nov-1991 #product Ig heavy chain V region #status predicted
#domain variable region #label VMC
11-Nov-1991 #length 124 #checksum 1710

Query Match
Best Local Similarity 10.0 #score 18; DB 2; Length 124;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 107 DYNOCGCTVTSANKTPP 124
OY 125 DYNOCGCTVTSANKTPP 142

RESULT 16

DB 130 DYNOCGCTVTSANKTPP 148
OY 125 DYNOCGCTVTSANKTPP 143

RESULT 14
ENTRY S29594 #type fragment
TITLE Ig heavy chain V region (fragment)
ORIGINISM 06-Jun-1995 #sequence_revision 06-Jun-1995 #text_change
DATE 06-Jun-1995
ACCESSIONS S29594
REFERENCES Seymour, R.
#journal submitted to the EMBL Data Library, February 1991
#abstract
#accession S29594
#molecule_type mRNA
#residues 1-130 #label ZEB
CLASSIFICATION #cross-reference EMBL:X3776; NID:954475; PID:954476
REMARKS #superfamily Immunoglobulin V region: Immunoglobulin homology
FEATURES
1-130 #domain signal sequence #status predicted #label SIGV
20-130 #product Ig heavy chain V region #status predicted
#domain variable region #label VMC
20-117 #length 152 #checksum 9709

Query Match
Best Local Similarity 10.0 #score 19; DB 2; Length 152;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 130 DYNOCGCTVTSANKTPP 148
OY 125 DYNOCGCTVTSANKTPP 143

RESULT 17
ENTRY S18950 #type complete
TITLE Ig heavy chain V region (clone 12d4) - mouse
ORIGINISM 23-May-1997
DATE 23-May-1997
ACCESSIONS S18950
REFERENCES Kallus, B.; Betel, G.; Shao, H.; Diamantstein, T.; Wiedle,
#journal gene (1992) 123:321-328
#abstract by inverse polymerase chain reaction which conserves
#accession S18950
#molecule_type mRNA
#residues 1-150 #label KAL
CLASSIFICATION #cross-reference G0:102316
REMARKS #superfamily Immunoglobulin V region: Immunoglobulin homology
FEATURES
1-150 #domain signal sequence #status predicted #label SIGV
20-150 #product Ig heavy chain V region #status predicted
#domain variable region #label VMC
20-117 #length 150 #checksum 9720

Query Match
Best Local Similarity 10.0 #score 19; DB 2; Length 150;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 103 DYNOCGCTVTSANKTPP 119

RESULT 17
ENTRY S18950 #type complete
TITLE Ig heavy chain V region (clone 12d4) - mouse
ORIGINISM 23-May-1997
DATE 23-May-1997
ACCESSIONS S18950
REFERENCES Kallus, B.; Betel, G.; Shao, H.; Diamantstein, T.; Wiedle,
#journal gene (1992) 123:321-328
#abstract by inverse polymerase chain reaction which conserves
#accession S18950
#molecule_type mRNA
#residues 1-150 #label KAL
CLASSIFICATION #cross-reference G0:102316
REMARKS #superfamily Immunoglobulin V region: Immunoglobulin homology
FEATURES
1-150 #domain signal sequence #status predicted #label SIGV
20-150 #product Ig heavy chain V region #status predicted
#domain variable region #label VMC
20-117 #length 150 #checksum 9720

Query Match
Best Local Similarity 10.0 #score 19; DB 2; Length 150;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 103 DYNOCGCTVTSANKTPP 119


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TITLE
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DATE
ACCESSION
AUTHOR
TITLE
REFERENCE
ACCESSION
SEQUENCE
STATUS
MOLECULE-TYPE
SEQUENCES
CLASSIFICATION
REMARKS
FEATURES
SUMMARY
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#Journal      D.: Marsha-Roberts, A.; Weigert, M.
#Title        J. Exp. Med. (1980) 171:265-297
#Accession    accession: P00742
#References    accession: P00742
#Keywords      #region 1-91, #stabil: SH2
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#Remarks      heterotrimeric; immunoglobulin
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#Region        1564-1571
#Region        1572-1579
#Region        1580-1587
#Region        1588-1595
#Region        1596-1603
#Region        1604-1611
#Region        1612-1619
#Region        1620-1627
#Region        1628-1635
#Region        1636-1643
#Region        1644-1651
#Region        1652-1659
#Region        1660-1667
#Region        1668-1675
#Region        1676-1683
#Region        1684-1691
#Region        1692-1699
#Region        1700-1707
#Region        1708-1715
#Region        1716-1723
#Region        1724-1731
#Region        1732-1739
#Region        1740-1747
#Region        1748-1755
#Region        1756-1763
#Region        1764-1771
#Region        1772-1779
#Region        1780-1787
#Region        1788-1795
#Region        1796-1803
#Region        1804-1811
#Region        1812-1819
#Region        1820-1827
#Region        1828-1835
#Region        1836-1843
#Region        1844-1851
#Region        1852-1859
#Region        1860-1867
#Region        1868-1875
#Region        1876-1883
#Region        1884-1891
#Region        1892-1899
#Region        1900-1907
#Region        1908-1915
#Region        1916-1923
#Region        1924-1931
#Region        1932-1939
#Region        1940-1947
#Region        1948-1955
#Region        1956-1963
#Region        1964-1971
#Region        1972-1979
#Region        1980-1987
#Region        1988-1995
#Region        1996-2003
#Region        2004-2011
#Region        2012-2019
#Region        2020-2027
#Region        2028-2035
#Region        2036-2043
#Region        2044-2051
#Region        2052-2059
#Region        2060-2067
#Region        2068-2075
#Region        2076-2083
#Region        2084-2091
#Region        2092-2099
#Region        2100-2107
#Region        2108-2115
#Region        2116-2123
#Region        2124-2131
#Region        2132-2139
#Region        2140-2147
#Region        2148-2155
#Region        2156-2163
#Region        2164-2171
#Region        2172-2179
#Region        2180-2187
#Region        2188-2195
#Region        2196-2203
#Region        2204-2211
#Region        2212-2219
#Region        2220-2227
#Region        2228-2235
#Region        2236-2243
#Region        2244-2251
#Region        2252-2259
#Region        2260-2267
#Region        2268-2275
#Region        2276-2283
#Region        2284-2291
#Region        2292-2299
#Region        2300-2307
#Region        2308-2315
#Region        2316-2323
#Region        2324-2331
#Region        2332-2339
#Region        2340-2347
#Region        2348-2355
#Region        2356-2363
#Region        2364-2371
#Region        2372-2379
#Region        2380-2387
#Region        2388-2395
#Region        2396-2403
#Region        2404-2411
#Region        2412-2
```

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Query Match      9.8i; Score 15; DB 2; Length 43;
Best Local Similarity 100.0%; Pred.No. 2,73e-16;
Matches 157 Conservative; 0 Mismatches 0 Indels 0 Gaps 0;

Db      4 SSTRSDSNAYVPCAR 18
|||||
QY      103 SSTRSDSNAYVPCAR 117

RESULT 25
ENTRY    H28833
ORIGIN   18 gaps fragment
ORGANISM Mus musculus common house mouse
DATE     30-Sep-1989
DB-KEY   1997
ACCESSIONS
REFERENCES
AUTHORS   Schmitt, C.; Rahn, M.; Roth, C.; These, J.; Fougerneau, M.;
          J. Imhoff, C.
          J. Immunol. (1988) 141:773-784
          Allogeneic manipulation of the CAT idiotype cascade.
          A stimulation of C5B/B6 mice by BALB/c anti-idiotypes
          against a strain specific V genes as the original
          antigen.
          Increases-reference NCID:88295674
          accession H28833 NMA
          #strides 1
          #residues 1 67 #state1 COP
          heterofamily immunoglobulin v region; immunoglobulin homology
          heterocenter family immunoglobulin
          strength 67 scoreksum 445

Query Match      9.8i; Score 15; DB 2; Length 67;
Best Local Similarity 100.0%; Pred.No. 2,73e-16;
Matches 151 Conservative; 0 Mismatches 0 Indels 0 Gaps 0;

Db      53 SSTRSDSNAYVPCAR 67
|||||
QY      103 SSTRSDSNAYVPCAR 117

RESULT 26
ENTRY    P10242
ORIGIN   15 heavy chain v region (anti-DNA, 554vH) - mouse (fragment)
ORGANISM Mus musculus common house mouse
DATE     18-Aug-1992
DB-KEY   sequence_revision 10-Sep-1992 text_change
ACCESSIONS
REFERENCES
AUTHORS   Stohlmacher, M.; Maccellini, M.; Shan, E.; Radic, M.Z.; Placastay,
          Stohlmacher, M.; Maccellini, M.; Shan, E.; Radic, M.Z.; Placastay,

```

[illegible]

```

#author      William D.M.;Jody N.T.;Hill, R.J.; Marion, T.N.
#journal     Journal of Molecular Evolution
#title       B-cell derived immunoglobulin antibodies are the products of
            both germ-line DNA rearrangement and somatic mutation. A
            clonally selective B cell stimulation in (NZB x NZW)F1
            mice.
#accession   PM1007
#molecule_type mRNA
#redundant   no
#sequences   1-106 #label titl
#experimental_source B cell, strain (NZB x NZW)F1
#superfamily Immunoglobulin V region; immunoglobulin homology
#interfamily Immunoglobulin
#features     length 106
            #domain immunoglobulin homology #label IMV
SUBMARY
Query Match          9 88: 9.88: 9.88: 9.88: 9.88: 9.88: 9.88: 9.88: 9.88: 9.88:
Beat Local Similarity 100.00: Pred. No. 2,73e-16:
Matches              15: Conservative           0: Mismatches           0: Indels           0: Gaps           0:
Db                   83 SSETSDSNAYVRAC 97
                    |||
                    |||
                    |||
                    |||
                    |||
Oy                  103 SSETSDSNAYVRAC 117

RESULT    30
ENTRY     19 H3040
TITLE     Ig heavy chain V region (anti-DNA, SJIVE) - mouse (fragment)
AUTHOR    [formal name] Mus musculus [common_name] house mouse
DATE      16-Aug-1996
ORIGIN    16-Aug-1996
REFERENCE P100310
AUTHORS   Shiohama, M.; Wessells, M.; Shan, H.; Radic, K.E.; Placzaky,
            B.D.; Maratschke-Buchstein, A.; Weigert, M.
JOURNAL   J. Exp. Med. (1990) 171:465-497
TITLE     Anti-DNA antibodies from autoimmune mice arise by clonal
            expansion and somatic mutation.
ACCESSION P100310
REFERENCE P100310
AUTHORS   *molecule-type mRNA
            #sequences 1-107 #label SHL
            #superfamily Immunoglobulin V region; immunoglobulin homology
FEATURES   Metastatements: Immunoglobulin
            #region framework 1\
            #domain immunoglobulin homology #label IMM
            #region framework 2\city-determining 1\
            #region complementarity-determining 2\
            #region framework 3\
55-86

```

```

87-97      #region complementarity-determining 3V
SUBALIGN   96-107    #region framework 4
            length 107 editCount=1469

Query Match          9.8% Score 15; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2,79e+16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 72 SLTSSDSGVAYPCOA 86
|||||
|||

QY 103 SLTSSDSGVAYPCOA 117

RESULT 31

ENTRY      PLOC241
TITLE      1B heavy chain V region (anti-DNA, S41VR) - mouse (fragment)
AUTHORS    Kozmichev, Y.; Maccoll, I. M.; Shih, H.; Riddick, M.T.; Placety,
DATE       J. Exp. Med. (1990) 171:285-297
JOURNAL     Antic-DNA antibodies from autoimmune mice arise by clonal
           expansion and somatic mutation.
ACCESSIONS accesion PLOC241
REFERENCES  PLOC241
REMARKS     *molecule type mRNA
           *residue 1-107 @label SHL
CLASSICCTON superfamily: Immunoglobulin V region; immunoglobulin homology
FEATURES
REGION      heterodomain; immunoglobulin
1-18        #region framework 3V
1-38        #domain immunoglobulin homology @label IMM
1-39        #region framework 3V
24-37       #region framework 3V; determining 3V
38-54       #region complementarity-determining 3V
55-86       #region framework 3V
87-107      #region complementarity-determining 3V
SIMMARY     #length 107 #checksum 7555

Query Match          9.8% Score 15; DB 2; Length 107;
Best Local Similarity 100.0%; Pred. No. 2,79e+16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 72 SLTSSDSGVAYPCOA 86
|||||
|||

QY 103 SLTSSDSGVAYPCOA 117
```

[illegible]

```

CLASSIFICATION      heterotetramerically immunoglobulin V region; immunoglobulin homology
KEYWORDS            heterotetramerically immunoglobulin V
FEATURE             1-36
SEQUENCE            *length 109 aminoAcids 7740

Query Match        9.8% Score 15; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 2,73e-16;
Matches           15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db                84 SALTSDSBNVCFA 98
OY               103 SALTSDSBNVCFA 117

RESULT            PH1000
ENTRY             19 heavy chain V region (clone 202.105) - mouse (fragment)
TITLE             19 heavy chain V region (clone 202.105) - mouse (fragment)
ACCESSION         J02205
DATE              30-Sep-1993 sequence_revision 30-Sep-1993 text_change 18-Aug-1996
ACCESSIONS       PH1000
REFERENCES         TILLMAN, D.M.; JOH, N.T.; HILL, R.J.; MARION, T.N.
                  J. Exp. Med. (1992), 176:761-779
                  Both IgM and IgG anti-DNA antibodies are the products of
                  clonally selective B cell stimulation in (NBS x NEM)F1
                  #title
#accession         PH1000
#description        Nucleic acid sequence not shown
#features           nucleic_acid_type mRNA
#analysis           #residue 1-110 label titl
#classification     heterotetramerically immunoglobulin V region; immunoglobulin homology
CLASSIFICATION     heterotetramerically immunoglobulin V region; immunoglobulin homology
KEYWORDS           heterotetramerically immunoglobulin V
FEATURE           1-110
SEQUENCE          *length 110 nucleotides 317

Query Match       9.8% Score 15; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 2,73e-16;
Matches           15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db                84 SALTSDSBNVCFA 98
OY               103 SALTSDSBNVCFA 117

RESULT            526317
ENTRY             #type fragment
```

TITLE 1g heavy chain V region - mouse (fragment)
 ORIGINISM 19-Mar-1998 sequence_revision 19-Mar-1998 text_change
 DATE 17-Apr-1998
 ACCESSIONS 525033
 REFERENCE 525030
 #authors Stark, S.E.; Caton, A.J.
 #journal J. Exp. Med. (1991) 174:613-624
 #title Antibodies that are specific for a single amino acid
 #abstract Antigenic determinants in a protein epitope use structurally distinct
 #molecule_type mRNA
 #residues 1-110 #label STR
 #cross-references EMBL:K51845; NID:953244; PTD:930213
 CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
 KEYWORDS heterotrimer; Immunoglobulin
 SUMMARY length 110 #checksum 513
 Query Match 9.8% Score 15; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2,73e-16;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 96 AIDYGCCTGYTSS 110
 ||||||||||||
 QY 123 AIDYGCCTGYTSS 137

RESULT 36
 ENTRY 525033
 TITLE 1g heavy chain V region (germline) center B17 DNA Nr.4 and
 ORIGINISM other(s) - mouse (fragment)
 DATE 25-Feb-1998 sequence_revision 01-Dec-1995 text_change
 ACCESSIONS 525033; 525035
 REFERENCE 525032
 #authors Jacob, J.; Kojima, G.
 #journal J. Biol. Chem. (1992) 267:11711-11717
 #title In situ studies on the primary immune response to
 #abstract submitted to the EMBL Data Library, July 1992
 #description In situ studies on the primary immune response to
 for perlecanin-1 lymphoid sheath associated foot and
 #molecule_type nucleic acid
 #residues 1-111 #label JMC
 #cross-references EMBL:K61770; NID:950079; PTD:944190; PTD:9333065
 #journal J. Biol. Chem. (1992) 267:11711-11717
 #title Variable region sequences of pathogenic anti-mouse red blood
 #abstract cell autoantibodies from autoimmune NZB mice
 #accession 525035
 #molecule_type nucleic acid
 #residues 1-111 #label JMC

RESULT 38
 ENTRY 509957
 TITLE 1g heavy chain V-D-J region (106-10P) - mouse (fragment)
 ORIGINISM formal_name Mus musculus scowon_name mouse
 DATE 12-Feb-1993 sequence_revision 12-Feb-1993 text_change
 ACCESSIONS 509957
 REFERENCE 509955
 #authors Rejzinger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton,
 #journal Eur. J. Immunol. (1990) 20:771-777
 #title Variable region sequences of pathogenic anti-mouse red blood
 #abstract cell autoantibodies from autoimmune NZB mice
 #accession 509957
 #molecule_type mRNA
 #residues 1-112 #label RET
 #cross-references EMBL:K51845; NID:953244; PTD:930213
 CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
 KEYWORDS heterotrimer; Immunoglobulin
 SUMMARY length 112 #checksum 334
 Query Match 9.8% Score 15; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 2,73e-16;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 14 SASVYSCASCTT 28
 ||||||||||||
 QY 33 SASVYSCASCTT 47

RESULT 39
 ENTRY 555535
 TITLE 1g heavy chain V region P23 - mouse (fragment)
 ORIGINISM formal_name Mus musculus scowon_name mouse
 DATE 08-Sep-1997 sequence_revision 01-Nov-1995 text_change
 ACCESSIONS 555535
 REFERENCE 555528
 #authors Jacob, J.; Kojima, G.; Caton, A.J.; Stark, S.E.; Spruce, B.A.
 #journal J. Exp. Med. (1991) 174:613-624
 #title Antibodies that are specific for a single amino acid
 #abstract Comprehensive epitope analysis of monoclonal
 anti-proteinase inhibitor antibodies using phage display libraries
 and synthetic peptides: revelation of antibody fine
 structure and identification of somatic mutations in the variable
 region genes.
 #accession 555535
 #status Preliminary
 #molecule_type mRNA

**cross-references EMBL:K61772; NID:950081; PTD:944192; PTD:9333067
 **experimental evidence antibody to B17 DNA Nr.6
 CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
 KEYWORDS heterotrimer; Immunoglobulin
 SUMMARY length 111 #checksum 6426
 Query Match 9.8% Score 15; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2,73e-16;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 80 SITSBSAVYPCAR 94
 ||||||||||||
 QY 103 SITSBSAVYPCAR 117

RESULT 37
 ENTRY 525034
 TITLE 1g heavy chain V region (germline) center B17 DNA Nr.4 and
 ORIGINISM formal_name Mus musculus scowon_name mouse
 DATE 19-Feb-1994 sequence_revision 01-Dec-1995 text_change
 ACCESSIONS 525034
 REFERENCE 525032
 #authors Jacob, J.; Kojima, G.
 #journal J. Biol. Chem. (1992) 267:11711-11717
 #title In situ studies on the primary immune response to
 #abstract submitted to the EMBL Data Library, July 1992
 #description In situ studies on the primary immune response to
 for perlecanin-1 lymphoid sheath associated foot and
 #molecule_type nucleic acid
 #residues 1-111 #label JMC
 #cross-references EMBL:K61771; NID:950081; PTD:944191; PTD:9333066
 CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
 KEYWORDS heterotrimer; Immunoglobulin
 SUMMARY length 111 #checksum 6414
 Query Match 9.8% Score 15; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2,73e-16;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 80 SITSBSAVYPCAR 94
 ||||||||||||
 QY 103 SITSBSAVYPCAR 117

**residues 1-113 #label BOB
 **cross-references EMBL:K61772; NID:954410; PTD:954411
 CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
 KEYWORDS heterotrimer; Immunoglobulin
 SUMMARY length 113 #checksum 3320
 Query Match 9.8% Score 15; DB 2; Length 113;
 Best Local Similarity 100.0%; Pred. No. 2,73e-16;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 84 SITSBSAVYPCAR 98
 ||||||||||||
 QY 104 SITSBSAVYPCAR 116

RESULT 40
 ENTRY A54376
 TITLE 1g heavy chain V region anti-tripleplex DNA - mouse (fragment)
 ORIGINISM formal_name Mus musculus scowon_name mouse
 DATE 06-Oct-1998 sequence_revision 16-Nov-1994 text_change
 ACCESSIONS A54376
 REFERENCE A54378
 #authors V.M.; Lee, J.S.; Bartholomew, G.D.
 #journal J. Biol. Chem. (1994) 269:11711-11717
 #title Characterization of a new monoclonal antibody to tripleplex
 #abstract and immunofluorescent staining of mammalian chromosomes.
 #accession A54376
 #status Preliminary
 #molecule_type mRNA
 #residues 1-115 #label AGA
 #cross-references EMBL:K61773; NID:954412; PTD:954413
 CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
 KEYWORDS heterotrimer; Immunoglobulin
 SUMMARY length 115 #checksum 7591
 Query Match 9.8% Score 15; DB 2; Length 115;
 Best Local Similarity 100.0%; Pred. No. 2,73e-16;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 84 SITSBSAVYPCAR 98
 ||||||||||||
 QY 103 SITSBSAVYPCAR 117

```
RESULT 41
ENTRY      PLO238      #type fragment
TITLE      Ig heavy chain V region (anti-DNA, 6NWH and 6QVH) - mouse
ORGANISM   Mus musculus (common name house mouse)
DATE       16-Sep-1992 sequence_revision 16-Sep-1992 text_change
REFERENCE   PLO238
AUTHORS     Shlomchik, M.; Marcello, M.; Shan, H.; Radic, M.Z.; Plasterky,
            J. Exp. Med. (1990) 171:265-297
            #journal Anti-DNA antibodies from autoimmune mice arise by clonal
            #title expansion and somatic mutation.
            #accession NCBI:00111618
            #molecule_type mRNA
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
FEATURES
FEATURE     1-30     #region framework 1\
             15-98   #domain immunoglobulin homology #label IMH\
             15-98   #region complementarity-determining 1\
             30-66   #region complementarity-determining 2\
             67-98   #region complementarity-determining 3\
             99-107   #region complementarity-determining 3\
             110-117 #checksum 6615
SUMMARY     #length 117 checksum 6615
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pctd. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
RESULT 42
ENTRY      PLO237      #type fragment
TITLE      Ig heavy chain V region (anti-DNA, 1A11YH) - mouse (fragment)
ORGANISM   Mus musculus (common name house mouse)
DATE       16-Sep-1992 sequence_revision 16-Sep-1992 text_change
REFERENCE   PLO237
AUTHORS     Shlomchik, M.; Marcello, M.; Shan, H.; Radic, M.Z.; Plasterky,
            J. Exp. Med. (1990) 171:265-297
            #journal Anti-DNA antibodies from autoimmune mice arise by clonal
            #title expansion and somatic mutation.
            #accession NCBI:00111618
            #molecule_type mRNA
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
FEATURES
FEATURE     1-30     #region framework 1\
             15-98   #domain immunoglobulin homology #label IMH\
             15-98   #region complementarity-determining 1\
             30-66   #region complementarity-determining 2\
             67-98   #region complementarity-determining 3\
             99-107   #region complementarity-determining 3\
             110-117 #checksum 6615
SUMMARY     #length 117 checksum 6615
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pctd. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
```

```
11-35     #region complementarity-determining 1\
16-49     #region framework 2\
50-66     #region complementarity-determining 2\
67-98     #region complementarity-determining 3\
110-117   #region complementarity-determining 3\
SUMMARY   #length 117 checksum 6657
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pctd. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
RESULT 44
ENTRY      PLO236      #type fragment
TITLE      Ig heavy chain V region (anti-DNA, 1A11YH) - mouse (fragment)
ORGANISM   Mus musculus (common name house mouse)
DATE       16-Sep-1992 sequence_revision 16-Sep-1992 text_change
REFERENCE   PLO236
AUTHORS     Shlomchik, M.; Marcello, M.; Shan, H.; Radic, M.Z.; Plasterky,
            J. Exp. Med. (1990) 171:265-297
            #journal Anti-DNA antibodies from autoimmune mice arise by clonal
            #title expansion and somatic mutation.
            #accession NCBI:00111618
            #molecule_type mRNA
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
FEATURES
FEATURE     1-30     #region framework 1\
             15-98   #domain immunoglobulin homology #label IMH\
             15-98   #region complementarity-determining 1\
             30-66   #region complementarity-determining 2\
             67-98   #region complementarity-determining 3\
             99-107   #region complementarity-determining 3\
             110-117 #checksum 6657
SUMMARY     #length 117 checksum 6657
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pctd. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
RESULT 45
ENTRY      PLO234      #type fragment
TITLE      Ig heavy chain V region (anti-DNA, 3B9VH) - mouse (fragment)
```

```
#title Anti-DNA antibodies from autoimmune mice arise by clonal
#accession NCBI:00111618
#molecule_type mRNA
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
FEATURES
FEATURE     1-30     #region framework 1\
             15-98   #domain immunoglobulin homology #label IMH\
             15-98   #region complementarity-determining 1\
             30-66   #region complementarity-determining 2\
             67-98   #region complementarity-determining 3\
             99-107   #region complementarity-determining 3\
             110-117 #checksum 6907
SUMMARY     #length 117 checksum 6907
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pctd. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
RESULT 43
ENTRY      PLO235      #type fragment
TITLE      Ig heavy chain V region (anti-DNA, 2P2VH and 4B9VH) - mouse
ORGANISM   Mus musculus (common name house mouse)
DATE       16-Sep-1992 sequence_revision 16-Sep-1992 text_change
REFERENCE   PLO235
AUTHORS     Shlomchik, M.; Marcello, M.; Shan, H.; Radic, M.Z.; Plasterky,
            J. Exp. Med. (1990) 171:265-297
            #journal Anti-DNA antibodies from autoimmune mice arise by clonal
            #title expansion and somatic mutation.
            #accession NCBI:00111618
            #molecule_type mRNA
CLASSIFICATION superfamily Immunoglobulin V region; Immunoglobulin homology
FEATURES
FEATURE     1-30     #region framework 1\
             15-98   #domain immunoglobulin homology #label IMH\
             15-98   #region complementarity-determining 1\
             30-66   #region complementarity-determining 2\
             67-98   #region complementarity-determining 3\
             99-107   #region complementarity-determining 3\
             110-117 #checksum 6907
SUMMARY     #length 117 checksum 6907
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pctd. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
RESULT 46
ENTRY      PLO231      #type fragment
TITLE      Ig heavy chain V region (anti-DNA, 2B9VH) - mouse (fragment)
ORGANISM   Mus musculus (common name house mouse)
DATE       16-Sep-1992 sequence_revision 16-Sep-1992 text_change
REFERENCE   PLO231
AUTHORS     Shlomchik, M.; Marcello, M.; Shan, H.; Radic, M.Z.; Plasterky,
            J. Exp. Med. (1990) 171:265-297
            #journal Anti-DNA antibodies from autoimmune mice arise by clonal
            #title expansion and somatic mutation.
            #accession NCBI:00111618
```

```
11-35     #region complementarity-determining 1\
16-49     #region framework 2\
50-66     #region complementarity-determining 2\
67-98     #region complementarity-determining 3\
110-117   #region complementarity-determining 3\
SUMMARY   #length 117 checksum 7994
Query Match 9.8% Score 15: DB 2: Length 117:
Best Local Similarity 100.0% Pctd. No. 2:73e-16:
Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 84 SBLTSDSNAYPCAR 98
CY 103 SBLTSDSNAYPCAR 117
RESULT 46
ENTRY      PLO231      #type fragment
TITLE      Ig heavy chain V region (anti-DNA, 2B9VH) - mouse (fragment)
ORGANISM   Mus musculus (common name house mouse)
DATE       16-Sep-1992 sequence_revision 16-Sep-1992 text_change
REFERENCE   PLO231
AUTHORS     Shlomchik, M.; Marcello, M.; Shan, H.; Radic, M.Z.; Plasterky,
            J. Exp. Med. (1990) 171:265-297
            #journal Anti-DNA antibodies from autoimmune mice arise by clonal
            #title expansion and somatic mutation.
            #accession NCBI:00111618
```

```

**molecule-type mRNA
**residues 1-118 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
DB 1-30
15-98 #region framework 1\
31-35 #domain immunoglobulin homology #label IMM
36-42 #region complementarity-determining 1\
43-52 #region complementarity-determining 2\
67-96 #region framework 2\
97-110 #region complementarity-determining 3\
111-118 #region framework 4\
SUMMARY #length 118 #checksum 4739
Query Match 9.84; Score 15; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 84 S5L7E8SNAVPCAR 98
111-118 #region framework 1\
119-126 #region framework 2\
127-134 #region framework 3\
135-142 #region framework 4\
SUMMARY #length 142 #checksum 4739
Query Match 9.84; Score 15; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 103 S5L7E8SNAVPCAR 117
**molecule-type mRNA
**residues 1-118 #label SHL
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
DB 1-30
15-98 #region framework 1\
31-35 #domain immunoglobulin homology #label IMM
36-42 #region complementarity-determining 1\
43-52 #region complementarity-determining 2\
67-96 #region framework 2\
97-110 #region complementarity-determining 3\
111-118 #region framework 4\
SUMMARY #length 118 #checksum 4739
Query Match 9.84; Score 15; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 84 S5L7E8SNAVPCAR 98
111-118 #region framework 1\
119-126 #region framework 2\
127-134 #region framework 3\
135-142 #region framework 4\
SUMMARY #length 142 #checksum 4739
Query Match 9.84; Score 15; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 103 S5L7E8SNAVPCAR 117

```

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Query Match 9.84; Score 15; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 104 PYWOGGCVTVSSAK 118
111-118 #region framework 1\
119-126 #region framework 2\
127-134 #region framework 3\
135-142 #region framework 4\
SUMMARY #length 142 #checksum 4739
Query Match 9.84; Score 15; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 103 S5L7E8SNAVPCAR 117
**molecule-type DNA
**residues 1-119 #label WIN
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
DB 1-30
15-98 #region framework 1\
31-35 #domain immunoglobulin homology #label IMM
36-42 #region complementarity-determining 1\
43-52 #region complementarity-determining 2\
67-96 #region framework 2\
97-110 #region complementarity-determining 3\
111-118 #region framework 4\
SUMMARY #length 118 #checksum 4739
Query Match 9.84; Score 15; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 87 S5L7E8SNAVPCAR 101
111-118 #region framework 1\
119-126 #region framework 2\
127-134 #region framework 3\
135-142 #region framework 4\
SUMMARY #length 142 #checksum 4739
Query Match 9.84; Score 15; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 103 S5L7E8SNAVPCAR 117

```

```

REFERENCE PH0087
#authors Schmitt, D.; Poch, O.; Feder, G.; Heinrich, G.F.; Kocher,
#journal Mol. Immunol. (1990) 27:1029-1038
#title Molecular diversity of monoclonal antibodies
#cross-references PMID:91042649
#accession PH0099
#molecule-type mRNA
#residues 1-119 #label SCH
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
DB 1-30
15-98 #region framework 1\
31-35 #domain immunoglobulin homology #label IMM
36-42 #region complementarity-determining 1\
43-52 #region complementarity-determining 2\
67-96 #region framework 2\
97-110 #region complementarity-determining 3\
111-118 #region framework 4\
SUMMARY #length 118 #checksum 8885
Query Match 9.84; Score 15; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 105 DYWOGGCVTVSSAK 119
111-118 #region framework 1\
119-126 #region framework 2\
127-134 #region framework 3\
135-142 #region framework 4\
SUMMARY #length 142 #checksum 8885
Query Match 9.84; Score 15; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 125 DYWOGGCVTVSSAK 139

```

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Query Match 9.84; Score 15; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 84 S5L7E8SNAVPCAR 98
111-118 #region framework 1\
119-126 #region framework 2\
127-134 #region framework 3\
135-142 #region framework 4\
SUMMARY #length 142 #checksum 8885
Query Match 9.84; Score 15; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 2,736-16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 103 S5L7E8SNAVPCAR 117

```

Search completed: Thu Apr 15 18:11:40 1999
Job time : 37 secs.

FT CHAIN 20 117 10 HEAVY CHAIN V REGION (10A).
 FT NON-TER 117 117
 SO SEQUENCE 117 AA: 12972 MW: 94100028 CRC32:
 Query Match 117 28: Score 11: DB 1: Length 117:
 Best Local Similarity 100.00: Pred. No. 1,546-09:
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 103 SLSITSESNVY 113
 Oy 103 SLSITSESNVY 113

RESULT 11 STANDARD: PRT: 117 AA.
 AC P06328:
 DT 01-JAN-1986 (REL. 06, CREATED)
 DT 21-JUL-1986 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 DE 10 HEAVY CHAIN PRECURSOR V REGION (VH558 B4).
 OS MUS MUSCULUS (MOUSE).
 CC EPIKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: RODENTIA.
 RP SEQUENCE FROM N.A.
 RA BOTHEWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESWARY K.,
 BA BALTIMORE D.C. (1981).
 DR PIR: A02035; M08584.
 DR HSP: P01810; 12HL.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT CHAIN 1 19 10 HEAVY CHAIN V REGION (VH558 B4).
 FT DOMAIN 20 49 FRANKMOR 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRANKMOR 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON-TER 117 117
 SO SEQUENCE 117 AA: 12834 MW: 8569285 CRC32:
 Query Match 7 28: Score 11: DB 1: Length 117:
 Best Local Similarity 100.00: Pred. No. 1,546-09:
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 103 SLSITSESNVY 113
 Oy 103 SLSITSESNVY 113

OS MUS MUSCULUS (MOUSE).
 OC EPIKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: RODENTIA.
 RP SEQUENCE FROM N.A.
 RA BOTHEWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESWARY K.,
 BA BALTIMORE D.C. (1981).
 DR PIR: A02035; M08584.
 DR HSP: P01810; 12HL.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT CHAIN 1 19 10 HEAVY CHAIN V REGION (VH558 B4).
 FT DOMAIN 20 49 FRANKMOR 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRANKMOR 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON-TER 117 117
 SO SEQUENCE 117 AA: 12921 MW: D5650000 CRC32:
 Query Match 7 28: Score 11: DB 1: Length 117:
 Best Local Similarity 100.00: Pred. No. 1,546-09:
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 103 SLSITSESNVY 113
 Oy 103 SLSITSESNVY 113

RESULT 11 STANDARD: PRT: 121 AA.
 AC P06328:
 DT 01-JAN-1986 (REL. 06, CREATED)
 DT 21-JUL-1986 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 DE 10 HEAVY CHAIN PRECURSOR V REGION (VH558 B4).
 OS MUS MUSCULUS (MOUSE).
 CC EPIKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: RODENTIA.
 RP SEQUENCE FROM N.A.
 RA BOTHEWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESWARY K.,
 BA BALTIMORE D.C. (1981).
 DR PIR: A02035; M08584.
 DR HSP: P01810; 12HL.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT CHAIN 1 19 10 HEAVY CHAIN V REGION (VH558 B4).
 FT DOMAIN 20 49 FRANKMOR 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRANKMOR 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON-TER 117 117
 SO SEQUENCE 117 AA: 12921 MW: D5650000 CRC32:
 Query Match 7 28: Score 11: DB 1: Length 117:
 Best Local Similarity 100.00: Pred. No. 1,546-09:
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 103 SLSITSESNVY 113
 Oy 103 SLSITSESNVY 113

RESULT 12 STANDARD: PRT: 117 AA.
 AC P01745:
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 DE 10 HEAVY CHAIN PRECURSOR V REGION (VH558 B4).
 OS MUS MUSCULUS (MOUSE).
 CC EPIKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: RODENTIA.
 RP SEQUENCE FROM N.A.
 RA BOTHEWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESWARY K.,
 BA BALTIMORE D.C. (1981).
 DR PIR: A02035; M08584.
 DR HSP: P01810; 12HL.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT CHAIN 1 19 10 HEAVY CHAIN V REGION (VH558 B4).
 FT DOMAIN 20 49 FRANKMOR 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRANKMOR 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON-TER 117 117
 SO SEQUENCE 117 AA: 13016 MW: D7120388 CRC32:
 Query Match 7 28: Score 11: DB 1: Length 117:
 Best Local Similarity 100.00: Pred. No. 1,546-09:
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 60 P01745: 70
 Oy 60 P01745: 70

REVISIONS.
 RA ZAVUT R., COHEN J., GIVOL D.:
 BA BALTIMORE D.C. (1980).
 CC - THIS SEQUENCE WAS TRANSLATED FROM AN mRNA ISOLATED FROM A
 CC WYELON THAT SECRETES IGG2B.
 DR PIR: A02027; GYMS11.
 DR HSP: P01810; 12HL.
 KW IMMUNOGLOBULIN V REGION.
 FT CHAIN 1 121
 FT NON-TER 121
 SO SEQUENCE 121 AA: 13135 MW: 2A6F80C CRC32:
 Query Match 7 28: Score 11: DB 1: Length 121:
 Best Local Similarity 100.00: Pred. No. 1,546-09:
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 70 LNDATSSVY 80
 Oy 80 LNDATSSVY 99

RESULT 15 STANDARD: PRT: 137 AA.
 AC P01355:
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 DE 10 HEAVY CHAIN PRECURSOR V REGION (VH558 B4).
 OS MUS MUSCULUS (MOUSE).
 CC EPIKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: RODENTIA.
 RP SEQUENCE FROM N.A.
 RA BOTHEWELL A.L.M., PASKIND M., RETH M., IMANISHI-KARI T., RAJESWARY K.,
 BA BALTIMORE D.C. (1981).
 DR PIR: A02035; M08584.
 DR HSP: P01772; 12HL.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT CHAIN 1 19 10 HEAVY CHAIN V REGION (VH558 B4).
 FT DOMAIN 20 49 FRANKMOR 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRANKMOR 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON-TER 117 117
 SO SEQUENCE 117 AA: 12921 MW: D5650000 CRC32:
 Query Match 7 28: Score 11: DB 1: Length 117:
 Best Local Similarity 100.00: Pred. No. 1,546-09:
 Matches 11: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 Db 103 SLSITSESNVY 113
 Oy 103 SLSITSESNVY 113

	RESULT	16			
AD	PROJ:HOUSE	ELI732	STANDARD:	PRT:	139 MA.
BT	NOV-86				
D7	21-JUL-1986 (REV. 01)	(CREATED)			
D7	21-JUL-1986 (REV. 01)	(LAST SEQUENCE UPDATED)			
DT	01-OCT-1986 (REV. 34)	(LAST ANNOTATION UPDATED)			
OS	MOS MEXICUS (HORSE)	IN REGION (B1-6 / 106-2).			
OC	EVALUATOR: METALON	CHORATA; VERTEBRATA; TETRAPODA; MANOLINI;			
CC	HYPERHIA; ROBERTA.				
RC	SEQUENCE FROM N.A.				
RK	STRAIN-C57BL/6;				
RX	REDLINE; 01234568				
BA	ROTHWELL A L.H., PARKING H., REIT H., TANISHI-KANI T., RAJESWARY K.				
CC	CRLT 21635-637(1201).				
-1-	THE B1-6 MD CHAIN RNA WAS CLONED FROM A HYBRIDOMA MAKING				
CC	ANTIBODIES TO THE HAMPTER (4-HYDROXY-3-NITROPHENYL)ACETYL (NBP				
DR	EMB1: J00522; G195115.				
DR	PIR: A02034; MEGS18.				
DR	NESP: P01810; LYHL.				
DR	NCBI:GLOABOBL1	1	REGION: SIGNAL.		
FT	SIGNAL	20	139		
FT	CHAIN	20	139		
FT	DOMAIN	20	49		
FT	DOMAIN	50	68		
FT	DOMAIN	60	84		
FT	DOMAIN	69	85		
FT	DOMAIN	86	117		
FT	DOMAIN	118	134		
FT	DISFOLD	118	134		
FT	DISFOLD	41	115		
FT	NON_TER	139	139		
Q	SEQUENCE	139 MA.	15419 NM;	DEBCCTD	GRC32;

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FT	DOVAIN	1	98	A SEGMENT.
FT	DOVAIN	95	104	D SEGMENT.
FT	DOVAIN	105	118	J SEGMENT.
FT	DISULFID	72	98	BY SIMILARITY.
FT	NON-TER	118	116	
SQ	SEQUENCE	118 M4:	12934 M4:	2DDICE77 CMC32.
Query Match		6.5%:	Score 10:	DA 1: Length 118:
Best Local Similarity		100.0%:	Pred. No. 3.41e-07:	
Matches	10:	Conservative:	Q:	Mismatches 0: Indels

[illegible]

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ID      HV09.MOUSE; STANDARD; PRT: 117 MA.
AC      201,751-81,2711.
DT      01-JUL-1989 (REL. 11.1 CREATED)
DE      01-NOV-1990 (REL. 16.1 LAST ANNOTATION UPDATE)
DS      NC HGVY CHAIN PRECURSOR IN REGION (186-1).
OS      MMS RECDLDS (MOUSE).
OC      EUTHERIA, ROENTHA.
RN      111
RP      SEQUENCE FROM H. A.
RC      STANLEY-CITL66, 148.
RA      BOOTHILL A.L.M., PASTERD M., RETH M., IMASHI-EKAI T., RAJESWARI
RL      BALTHORST D.; CELL 34:825-637(1991).
RR      -1. THIS GENE/LOCUS BELONGS TO A SET OF CLOSELY RELATED GENES
CC      WITH SIMILAR NAMES IN REGIONS OF NBD ANTIBODIES.
CD      PIR: D02031; RMH651.
CM      HSBP; P01810; IPRB.
DR      HMHROGLOBULIN IN REGION; SIGNAL.
RW      1
RM      CHAIN L.
FT      DOMAIN 20 117
FT      DOMAIN 20 49
FT      DOMAIN 30 52
FT      DOMAIN 35 58
FT      DOMAIN 35 64
FT      DOMAIN 36 68
FT      DOMAIN 86 111
FT      DISULFED 41 115
FT      NON_TER 117 117
SQ      SEQUENCE 117 AA: 12890 MW: 6976832 CMC12;
        6.5%; Score 10. DB 1; Length 117;
        Best Local Similarity 100.0%; Pred. No. 3,44e-07;
Matches 10; Complement 0; Mismatches 0; Indels 0; Gaps 0
DB      92 PRSSSTATIO 101
       92 DISSTATIO 101

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[illegible]

RA	PCR	0.0	0.0/1.0	
RA	BIODIFF	0.1574449	4539(1976).	
CC	CC	-1	THIS STRAIN WAS OBTAINED FROM ANTIBODY TO TYPE III PNEUMOCOCCI	
CC	CC	-1	AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.	
DR	PIR	AD10103	CAS911.	
DR	PIR	AD10103	CAS911.	
RM	RM	IMMUNOCOMMUNITY	V REGION.	
PT	PT	NOL.RES	114	1
PT	PT	NOL.RES	114	1
SO	SEQUENCE	114 AA.	12335 NW.	69BBA079 CMC13.
				PYRROLIDONE CARBOXYLIC ACID.
	Query Match	5.98.	Score 9. ID: 1	Length 114.
	Best Local Similarity	88.99.	Pctd No. 5.92e-05.	
	Matches	8.	Mismatches	0.
DB	40	PGCAGLEMC	48	
		1111111111		
QY	60	PGCAGLEMC	68	
RESULT	21			

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FT DOMAIN 55 68 FRAMEWORK 2
FT DOMAIN 65 85 FRAMEWORK 3
FT DOMAIN 118 127 COMPLEMENTARITY DETERMINING 3.
FT DOMAIN 128 138 FRAMEWORK 4
FT DOMAIN 138 148 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA: 15976 MW: BFF6247B CRC32:
Query Match 5.2%: Score 8: DB 1: Length 138:
Best Local Similarity 100.0%: Pred. No. 7.61e-03:
Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 60 PROCELENTIC 68
QY 60 PROCELENTIC 68

RESULT 27
ID HVJ3.JRMAN STANDARD: PRT: 117 AA.
AC P13180.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
DE 1-CELL RECEPTOR ALPHA CHAIN V-1 REGION (H03).
OC HOMO SAPIENS (HUMAN).
OC EDUARDON: METALON: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN 111
RP SEQUENCE FROM N.A.
RA MEDLINE: 83144028.
RA RECHAVY G., RAM D., GLAZER L., ZARUT R., GYOL D.,
RA PROC. NATL. ACAD. SCI. U.S.A. 80:855-859(1983).
DR ENBL: X07448.
DR HSP: P01810.1979.
DR IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 19
FT NON_TER 20 117 IG HEAVY CHAIN V REGION (H03).
FT DOMAIN 117 117
SQ SEQUENCE 117 AA: 12946 MW: BCC8B1DB CRC32:
Query Match 5.2%: Score 8: DB 1: Length 117:
Best Local Similarity 100.0%: Pred. No. 7.61e-03:
Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 40 SCVASCIT 47
QY 40 SCVASCIT 47

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RX MEDLINE: 88294408.
RX MONTANA F., LEE R.H., NAKAI S., SATO T., KODAMA M., ZONG S.O.,
RX ENBL: X07448.
RX HSP: P01810.1979.
RX IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 19
FT NON_TER 20 117 IG HEAVY CHAIN V REGION (V35).
FT DOMAIN 117 117
SQ SEQUENCE 117 AA: 13009 MW: FFA56D01 CRC32:
Query Match 5.2%: Score 8: DB 1: Length 117:
Best Local Similarity 100.0%: Pred. No. 7.61e-03:
Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 40 SCVASCIT 47
QY 40 SCVASCIT 47

RESULT 30
ID TVAI.MOZE STANDARD: PRT: 110 AA.
AC P01738.1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE 1-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (PH0558).
OC MUS MUSCULUS (MURUS).
OC EDUARDON: METALON: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN 111
RP SEQUENCE FROM N.A.
RA MEDLINE: 83086254.
RA SATO H., FRANK D.M., TAKAGAKI Y., HAYDAY A.C., EISEN H.N.,
RA TOREKAWA S.:
RA NATURE 312:36-40(1984).
DR HSP: P01607.1985.
DR PIR: A02012.1985.
DR HSP: P01607.1985.
FT SIGNAL 21 110 T-CELL RECEPTOR ALPHA CHAIN V REGION.
FT DOMAIN 115 110 J SEQUENCE.
FT NON_TER 115 110
FT CARBONIED 130 130
SQ SEQUENCE 130 AA: 14320 MW: BFF7897B CRC32:

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ID HV01.CANAD STANDARD: PRT: 117 AA.
AC P13180.
DT 01-NOV-1990 (REL. 16, CREATED)
DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE 1-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (3).
OC CANISUS AURATUS (GOLDEN).
OC EDUARDON: METALON: CHORDATA: VERTEBRATA: PISCES: GNAITHOSTOMATA.
OC OSTEIFICHES: ACTINOPTERYGII: CYPRINIFORMES.
RN 111
RP SEQUENCE FROM N.A.
RA MEDLINE: 88144476.
RA WILSON M.R., MIDDLETON D., WARR G.W.:
RA ENBL: X01616.
RA PROC. NATL. ACAD. SCI. U.S.A. 85:1566-1570(1988).
DR PIR: A28966.
DR HSP: P01772.2784.
DR IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 20 117
FT NON_TER 20 117 IG HEAVY CHAIN V REGION (3).
FT DOMAIN 50 54 FRAMEWORK 1.
FT DOMAIN 55 58 COMPLEMENTARITY DETERMINING 1.
FT DOMAIN 58 68 FRAMEWORK 2.
FT DOMAIN 68 117 COMPLEMENTARITY DETERMINING 2.
FT DISULFD 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 13220 MW: A85C6F5 CRC32:
Query Match 5.2%: Score 8: DB 1: Length 117:
Best Local Similarity 100.0%: Pred. No. 7.61e-03:
Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 40 SCVASCIT 47
QY 40 SCVASCIT 47

RESULT 29
ID HVJ3.JRMAN STANDARD: PRT: 117 AA.
AC P13180.
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 20, LAST ANNOTATION UPDATE)
DE 1-CELL RECEPTOR ALPHA CHAIN PRECURSOR V-1 REGION (V35).
OC HOMO SAPIENS (HUMAN).
OC EDUARDON: METALON: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN 111
RP SEQUENCE FROM N.A.

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Query Match 5.2%: Score 8: DB 1: Length 130:
Best Local Similarity 100.0%: Pred. No. 7.61e-03:
Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 104 DSAVYFCA 111
QY 104 DSAVYFCA 116

RESULT 31
ID TVAI.MOZE STANDARD: PRT: 131 AA.
AC P01738.1986 (REL. 05, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 13-AUG-1987 (REL. 05, LAST ANNOTATION UPDATE)
DE 1-CELL RECEPTOR ALPHA CHAIN PRECURSOR V REGION (H03-HLT) (FRAMEWORK).
OC MUS MUSCULUS (MURUS).
OC EDUARDON: METALON: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
OC EUTHERIA: PRIMATES.
RN 111
RP SEQUENCE FROM N.A.
RA MEDLINE: 85086254.
RA SIM G.K., YAGUZ J., NELSON J., MARACK P., PALMER E., AUGUSTIN A.,
RA KAPPLER J.:
RA NATURE 312:771-776(1984).
DR HSP: P01607.1985.
DR PIR: A02012.1985.
DR HSP: P01607.1985.
FT SIGNAL 21 130 T-CELL RECEPTOR ALPHA CHAIN V REGION.
FT DOMAIN 116 131 J SEQUENCE.
FT NON_TER 116 131
FT CARBONIED 130 130
SQ SEQUENCE 131 AA: 14771 MW: D7D6CA3 CRC32:
Query Match 5.2%: Score 8: DB 1: Length 131:
Best Local Similarity 100.0%: Pred. No. 7.61e-03:
Matches 8: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
DB 105 DSAVYFCA 112
QY 105 DSAVYFCA 116

RESULT 32
ID TVAI.MOZE STANDARD: PRT: 135 AA.
AC P01738.1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)

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ID      YC9A_METNA STANDARD:          PRT:   254 AA.
CP      PS138:
DT      15-JUL-1998 (REL. 36, CREATED)
DD      DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATED)
DN      DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DE      HYPOTHETICAL PROTEIN M1287.1.
OS      M1287.1.
SC      METANAROCCLUS JANNASCHII.
OR      (M1287.1) ERMINGHAM, METNA; METNAROCOCCALES; METNAROCOCCACEAE.
RN      NCBI.
RC      STRAIN=JAL-1 / DSM 2657 / ATCC 43067.
RK      MEDLINE: 9631995. OLSEN G.J., BRUCE L., RICHARDSON A.D.,
RA      SUTTON C.G., BLAKE J.A., PITTSBURGH B., COOKEYE J.D.,
RA      KIRKHAUSE A.R., ROBERTS B.A., TOMI J.-F., ADAMS N.D., REICH C.I.,
RA      EVERHARTER K., KIRKNESS E.F., WEINSTEIN K.G., MERICK T.M., GLIDER A.,
RA      SCOTT J.T., GOODMAN N.S.H., WELDON J.F., FURMAN J.L., NOVEN D.,
RA      COTTON M.D., ROBERTS J.W., HENDERSON J., ALLEN S.O., PANDOLFEN N.C.,
RA      KLEIN H.-P., FRANK C.N., SMITH H.O., MOSE C.R., ZWIER J.C.,
RA      SCIENCE 273:1059-1074(1996).
CC      1 - SUPERLUMES LOCATION: INTERAL MEMBRANE PROTEIN (POTENTIAL),
CC      EMBL: G61546 (ATCC 43067); XNMACHCHI M1287.1.
DR      DR HTM: M1287.1.
KN      KN HYPOTHETICAL PROTEIN: TRANSMEMBRANE.
FT      TRANSMEN 33 53 POTENTIAL.
FT      TRANSMEN 50 110 POTENTIAL.
FT      TRANSMEN 90 110 POTENTIAL.
FT      TRANSMEN 133 153 POTENTIAL.
FT      TRANSMEN 223 233 POTENTIAL.
SQ      SEQUENCE 254 AA: 29365 MW: 0263CD CRC32:
        Query Match 4.6% Score 7. DB 1: length 254;
        Blast Local Similarity 100.0% Pfad No. 6,73e+01 Indels 0;
        Matches 7: Conservative 0; Mismatches 0; Gaps 0

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ID DIBOJ.BAT STANDARD. PRG: 273 AA
 RC POS987. 068478. 09. CHAETED
 DT 01.-P28-1393 (REL. 17. LAST SEQUENCE UPDATE)
 DT 15.-P29-1399 (REL. 36. LAST ANNOTATION UPDATE)
 DE NAD(P)H DEHYDROGENASE (GUINONE) (P. 1.6.99.3) (GUINONE REDUCTASE) (DT
 D2 DIAPHRASE) (AAROCEDOXINASE) (PHILLOQUINONE REDUCTASE) (NEMADIN
 G8 NMOL)
 CC RATTUS NORVEGICUS (BAT)
 CC EUMAROTIA. METASOA. CHORDATA. VERTEBRATA. TETRAPODA. MAMMALIA:
 CC EUTHERIA. ROENTHA.
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RP 1155D5-LAYER.
 RX MEDLINE: 81019147
 RX MEDLINE: 82043752
 RL J. BIOL. CHEM. 263:572-576(1987).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 50094356
 RX MEDLINE: 50094356
 RL J. BIOL. CHEM. 264:21793-21797(1989).
 RA BAYER R.M., MORROW M.R., PAVELAU L.V., PICKETT C.B.:
 RL 1155D5-LAYER.
 RX SEQUENCE FROM N.A.
 RX MEDLINE: 87057124.
 RA ROBERTSON J.A., CHEN H.-C., NIEBET D.W.:
 RL J. BIOL. CHEM. 261:15796-15799(1986).
 RP SEQUENCE.
 RX MEDLINE: 89062419.
 RA HANU M., TOUN H., CHEN S., TANAGI T., LEE T.D., SHEVEL J.E.:
 RL J. NEUROCHEMIST. 27:687-689(1986).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA ROBERTSON J.A., NIEBET D.W., HANTRINSON O.:
 RL J. GEN. SER. 27:83-87(1987).
 RP SEQUENCE OF 1-56 FROM N.A.
 RN [6]
 RA ARCH. BIOCHEM. BIOPHYS. 260:847-850(1988).
 RN [7]
 RX HOMOGENIS.
 RX MEDLINE: 00023064
 RA PORTER G.E., GIAN Y., MA J.-X., EAPLAN M.D., ABRAH S., DOROSHOW J.,
 CHEN S.:
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 169:1087-1093(1990).

[illegible]

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FT  MOTNAGE      163      163      D->O (DIETARY INTAKE).
CC  CONFLICT     134      134      K -> Q (IN REEF 11).
SQ  SEQUENCE     273 MA: 30815 MW: 30851V CIRC32:
Query Match      4.6% Score 7: DA 1: Length 273:
Beat Local Similarity 100.0% Pctd. No. 6.7e-01:
Matches          0: Conservative          0: Indels          0: Gaps
OY  10 LASTING  149
DB  143 LASTING  149
1111111
ID  BIRQU MOORE  STANDARD:      PRT:  273 MA.
RESULT  50
AC  Q41669:      1497 REEL  35 (CHARTED)
DC  Q41669:      1497 REEL  35 (CHARTED)
DT  01-NOV-1993 (REL. 35, LAST SEQUENCE UPDATE)
DT  15-NOV-1993 (REL. 36, LAST ANNOTATION UPDATE)
ND  P(PI)-299 (CHROM. 36, LAST ANNOTATION UPDATE)
DE  DIAPHORASE (ALDOREDOXINASE) (PHYLLODOXINONE REDUCTASE) (NEMATOXIN)
GN  NEMOLOXIN
GC  NEMOLOXIN
OS  MOS MOSCULUS (MORCUL).
OC  ERYTHROCYTES.
CC  ERYTHROCYTES. NEMATOXIN. CHROMATIN. VERTICILLATA. TETRAPODA. MAMMALIA.
CC  ERYTHROCYTES. NEMATOXIN.
RN  11
RP  SEQUENCE FROM N. A.
RC  STRAIN: Q318L/6 X CHM. TISSUE: LIVER.
RC  MEDLINE: 95128831 (GENE. 3).
RC  JOURNAL: J. GEN. PHYSIOL. 106: 1-10 (1994).
RL  PHARMACOCHEMISTS 41941-348 (1994).
RN  12
RP  SEQUENCE FROM N. A., AND PARTIAL SEQUENCE.
RC  MEDLINE: 95078131.
RC  JOURNAL: J. GEN. PHYSIOL. 106: 1-10 (1994).
RA  CHEN S. C., CLARK P. E., MARTINO P. A., DENG P. S., YEH C. H., LEE T. D.,
RA  PHOTONIS H. J., TALALY P.:
CC  PHOTOGRAPHIC RECORDING OF APPARENTLY SENSITIVE AS A GUTINONE REDUCTASE IN
CC  DETOXICATION PATHWAYS AS WELL AS IN BIOSYNTHETIC PROCESSES SUCH AS
CC  THE VITAMIN K-DEPENDENT GAMMA-CARBOXYLATION OF GLUTAMYLIC RESIDUES
CC  IN CONNECTION WITH CONJUGATION OF GLUTAMYLIC RESIDUES
CC  -1- ACCEPTOR: NAD(P)H + ACCEPTOR + NAD(P)(+)+ REDUCED
CC  ACCEPTOR.
CC  -1- CORYLORIN. PND FLAVONOLIN
CC  -1- CORYLORIN. PND FLAVONOLIN
CC  -1- SUPPLEMENTAL INFORMATION.
CC  -1- SUPPLEMENTAL INFORMATION.
CC  -1- INDUCTION: BY POLYCYCLIC HYDROCARBONS SUCH AS DIOXIN (GOVERNED BY
CC  THE AROMATIC HYDROCARBON RESPONSE) (AH1 LOCUS).

```

CC EMBL: 012961: G595510
 DR EMBL: 575951: G913763
 DR KGD: M6110187: NCOR1
 FT UNIPROT: P08000: NAD: NADP: FLAVOPROTEIN: FAD: ACETYLATION.
 FT MOD_RES 1 0
 SQ SEQUENCE 273 AA: 30828 MW: 8603955 CMC12:

Query Match 1.64 Score 7: DB 1: Length 273:
 Best Local Similarity 100.0%
 Matches 7: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

DB 143 LISTING 149
 QY 10 LISTING 16

Search completed: Thu Apr 15 16:09:11 1999
 Job time: 53 secs.

!!SEQUENCE_LIST 1.0
(Peptide) WORDSEARCH of: /home/obryen/ree455/olig/us-08-836-455-4 check: 265 from: 1

FROM: of: /home/obryen/ree455/olig/us-08-836-455-4
sequence 4, application us/08836455

general information:
applicant: chatterjee, malaya
applicant: foon, kenneth a.
applicant: chatterjee, sunil k. . .

TO: swp:* Sequences: 254,782 Total-length: 82,009,484 April 18, 1999 19:50

Database Release Information:

2 db's { SWISS-PROT, Release 36.0, Released on 18Jul1998, Formatted on 18Aug1998
SPREMBL, Release 8.0, Released on 21Nov1998, Formatted on 15Dec1998

Word-size: 5 Words: 52398 Diagonals: 10,097 Total Diagonals: 120,736,348
Integral-width: 1 Alphabet: 20 List-size: 50 CPU minutes: 9.48

Sequence SIRD Diag Score Width Documentation ..

SM:HV06_MOUSE	+	0	66	1	P01750 mus musculus (mouse). 1g heavy
SM:HV02_MOUSE	+	0	64	1	P01746 mus musculus (mouse). 1g heavy
SM:HV14_MOUSE	+	0	61	1	P01758 mus musculus (mouse). 1g heavy
SM:HV03_MOUSE	+	-20	58	1	P01747 mus musculus (mouse). 1g heavy
SM:HV09_MOUSE	+	0	56	1	P01753 mus musculus (mouse). 1g heavy
SM:HV05_MOUSE	+	0	56	1	P01749 mus musculus (mouse). 1g heavy
SM:HV52_MOUSE	+	0	56	1	P06327 mus musculus (mouse). 1g heavy
SM:HV49_MOUSE	+	0	55	1	P06328 mus musculus (mouse). 1g heavy
SM:HV07_MOUSE	+	0	54	1	P01751 mus musculus (mouse). 1g heavy
SM:HV04_MOUSE	+	0	52	1	P01748 mus musculus (mouse). 1g heavy
SM:HV13_MOUSE	+	-19	51	2	P01757 mus musculus (mouse). 1g heavy
SM:HV12_MOUSE	+	-19	51	2	P01756 mus musculus (mouse). 1g heavy
SM:HV11_MOUSE	+	0	50	1	P01755 mus musculus (mouse). 1g heavy
SM:HV51_MOUSE	+	-19	47	1	P06330 mus musculus (mouse). 1g heavy
SM:HV10_MOUSE	+	0	46	1	P01754 mus musculus (mouse). 1g heavy
SM:HV15_MOUSE	+	0	38	2	P01759 mus musculus (mouse). 1g heavy
SM:HV01_MOUSE	+	-19	36	1	P01745 mus musculus (mouse). 1g heavy
SM:HV00_MOUSE	+	-19	34	1	P01741 mus musculus (mouse). 1g heavy
SM:HV48_MOUSE	+	0	33	2	P03980 mus musculus (mouse). 1g heavy
SM:HV1G_HUMAN	+	0	30	1	P23083 homo sapiens (human). 1g heavy
SM:HV1B_HUMAN	+	-19	25	1	P01743 homo sapiens (human). 1g heavy
SM:HV50_MOUSE	+	-19	25	1	P06329 mus musculus (mouse). 1g heavy
SM:HV1C_HUMAN	+	-4	18	1	P01744 homo sapiens (human). 1g heavy
SM:HV1A_HUMAN	+	-19	18	2	P01742 homo sapiens (human). 1g heavy
SP:HM:015224	+	-110	18	1	O15224 homo sapiens (human). 1g heavy
SM:HV43_MOUSE	+	-1	14	1	P01819 mus musculus (mouse). 1g heavy
SM:HV16_MOUSE	+	-1	13	1	P01783 mus musculus (mouse). 1g heavy
SM:HV02_XENLA	+	-2	13	1	P20957 xenopus laevis (african clawed
SM:HV37_MOUSE	+	-19	12	1	P01807 mus musculus (mouse). 1g heavy
SM:HV42_MOUSE	+	-20	12	2	P01812 mus musculus (mouse). 1g heavy
SM:HV40_MOUSE	+	-19	12	1	P01810 mus musculus (mouse). 1g heavy
SM:HV3K_HUMAN	+	-11	12	1	P01772 homo sapiens (human). 1g heavy
SM:HV3G_HUMAN	+	-15	11	1	P01768 homo sapiens (human). 1g heavy
SM:HV38_MOUSE	+	-19	11	1	P01808 mus musculus (mouse). 1g heavy
SM:HV2C_RABBIT	+	-1	11	1	P01829 oryctolagus cuniculus (rabbit)
SM:HV2C_HUMAN	+	-18	11	1	P01816 homo sapiens (human). 1g heavy
SM:HV1E_HUMAN	+	-15	11	1	P01761 homo sapiens (human). 1g heavy
SM:HV1D_HUMAN	+	-15	11	1	P01760 homo sapiens (human). 1g heavy
SM:HV03_CALICR	+	0	11	1	P03962 calman crocodilus (spectacled
SM:HV01_RAT	+	5	11	1	P01805 rattus norvegicus (rat). 1g he
SP:HM:015224	+	-23	11	1	P01784 canis familiaris (dog). 1g he
SP:HM:015224	+	-125	11	1	P78465 homo sapiens (human). 1g heavy
SM:HV41_MOUSE	+	-19	11	2	P01811 mus musculus (mouse). 1g heavy
SM:HV3J_HUMAN	+	-16	11	1	P01771 homo sapiens (human). 1g heavy
SM:HV3I_HUMAN	+	-18	10	1	P01770 homo sapiens (human). 1g heavy
SM:HV3B_HUMAN	+	-23	10	1	P01763 homo sapiens (human). 1g heavy
SM:HV2I_HUMAN	+	9	10	1	P06331 homo sapiens (human). 1g heavy
SM:HV2D_HUMAN	+	-12	10	1	P01817 homo sapiens (human). 1g heavy
SM:HV1C_HUMAN	+	6	10	1	P01744 homo sapiens (human). 1g heavy
SM:HV3U_HUMAN	+	-17	10	1	P01782 homo sapiens (human). 1g heavy

of days computing matrices at least 5 or longer

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968 5 3.3 3011 14 081754 POLYPROTEIN 1.66e+03
 969 5 3.3 3011 14 036608 POLYPROTEIN 1.66e+03
 970 5 3.3 3011 14 036610 POLYPROTEIN 1.66e+03
 971 5 3.3 3011 14 036609 POLYPROTEIN 1.66e+03
 972 5 3.3 3021 14 081849 GENES FOR COX2, ENVELO 1.66e+03
 973 5 3.3 3021 14 081850 POLYPROTEIN 1.66e+03
 974 5 3.3 3022 14 081858 POLYPROTEIN 1.66e+03
 975 5 3.3 3022 14 081878 POLYPROTEIN 1.66e+03
 976 5 3.3 3053 14 071363 POLYPROTEIN 1.66e+03
 977 5 3.3 3053 14 071363 POLYPROTEIN 1.66e+03
 978 5 3.3 3053 14 071363 POLYPROTEIN 1.66e+03
 979 5 3.3 3053 14 071363 POLYPROTEIN 1.66e+03
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 999 5 3.3 3053 14 071363 POLYPROTEIN 1.66e+03
 1000 5 3.3 3053 14 071363 POLYPROTEIN 1.66e+03

ALIGNMENTS

RESULT 1
 ID 009199 PRELIMINARY: PRT: 118 AA.
 AC 009199: (REMBL: 04, CREATED)
 DT 01-JUN-1997 (REMBL: 04, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (REMBL: 06, LAST ANNOTATION UPDATE)
 DE IGM HEAVY CHAIN (FRAGMENT).
 OS UNKNOWN.
 OC UNCLASSIFIED.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN (REMBL: P1 MOUSE; TISSUE=SPLEEN;
 NC PAYELLE-BROCARD B.;
 RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.

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OS MUS MUSCULUS (MOUSE).
 OC EUTHERIA: RODENTIA.
 OC EUTHERIA: RODENTIA.
 RX MEDLINE: 96166461.
 RA KIMURA H., YOSHIMURA H., TANAKA K., SATOHARA T., KASAI F., ITOI S.,
 DR EMBL: S82857, G153586.
 DR PFM: PFM0047, 19.
 FT NON_TER 1 1
 SQ SEQUENCE 120 AA: 32A54DB8 CRC32:
 Query Match 9.2% Score 14: DB 11: Length 120:
 Best Local Similarity 100.0% Pred. No. 1.10e-17:
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 DB 14 GASTRASCASGTT 27
 QY 34 GASTRASCASGTT 47
 RESULT 4
 ID P70173 PRELIMINARY: PRT: 138 AA.
 AC P70173: (REMBL: 02, CREATED)
 DT 01-FEB-1997 (REMBL: 02, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (REMBL: 06, LAST ANNOTATION UPDATE)
 DE OKT3 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUTHERIA: RODENTIA.
 OC EUTHERIA: RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 97058313.
 RA KIMURA H., YOSHIMURA H., TANAKA K., SATOHARA T., KASAI F., ITOI S.,
 DR EMBL: D87081, G1565186.
 DR PFM: PFM0047, 19.
 FT SIGNAL 1 19
 FT CHAIN 20 >138
 SQ SEQUENCE 138 AA: 15648 MW: 7350DD0A CRC32:
 Query Match 9.2% Score 14: DB 11: Length 138:
 Best Local Similarity 100.0% Pred. No. 1.10e-17:
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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DR EMBL: U44924; G1763745.
 DR PFM: PFM0047, 19.
 FT NON_TER 1 1
 SQ SEQUENCE 118 AA: 13117 MW: 098386C5 CRC32:
 Query Match 9.8% Score 15: DB 11: Length 118:
 Best Local Similarity 100.0% Pred. No. 2.08e-20:
 Matches 15: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 DB 84 SBTSESNAYVCAR 98
 QY 103 SBTSESNAYVCAR 117
 RESULT 2
 ID 009200 PRELIMINARY: PRT: 118 AA.
 AC 009200: (REMBL: 04, CREATED)
 DT 01-JUN-1997 (REMBL: 04, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (REMBL: 06, LAST ANNOTATION UPDATE)
 DE IGM HEAVY CHAIN (FRAGMENT).
 OS UNKNOWN.
 OC UNCLASSIFIED.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN (REMBL: P1 MOUSE; TISSUE=SPLEEN;
 NC PAYELLE-BROCARD B.;
 RL SUBMITTED (JAN-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 DR EMBL: U44925; G1763747.
 DR PFM: PFM0047, 19.
 FT NON_TER 1 1
 SQ SEQUENCE 118 AA: 12937 MW: FF70A07 CRC32:
 Query Match 9.8% Score 14: DB 11: Length 118:
 Best Local Similarity 100.0% Pred. No. 1.10e-17:
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 DB 15 GASTRASCASGTT 28
 QY 34 GASTRASCASGTT 47

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OS MUS MUSCULUS (MOUSE).
 OC EUTHERIA: RODENTIA.
 OC EUTHERIA: RODENTIA.
 RX MEDLINE: 96166461.
 RA KIMURA H., YOSHIMURA H., TANAKA K., SATOHARA T., KASAI F., ITOI S.,
 DR EMBL: S82857, G153586.
 DR PFM: PFM0047, 19.
 FT NON_TER 1 1
 SQ SEQUENCE 120 AA: 32A54DB8 CRC32:
 Query Match 9.2% Score 14: DB 11: Length 120:
 Best Local Similarity 100.0% Pred. No. 1.10e-17:
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 DB 14 GASTRASCASGTT 27
 QY 34 GASTRASCASGTT 47
 RESULT 5
 ID P97467 PRELIMINARY: PRT: 111 AA.
 AC P97467: (REMBL: 03, CREATED)
 DT 01-MAY-1997 (REMBL: 03, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (REMBL: 06, LAST ANNOTATION UPDATE)
 DE OKT3 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUTHERIA: RODENTIA.
 OC EUTHERIA: RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 97257994.
 RA ITO H.O., UEDA T., IMOTO T., KOGA T.,
 DR EMBL: M01458, G151665.
 DR PFM: PFM0047, 19.
 FT NON_TER 1 1
 SQ SEQUENCE 111 AA: 12444 MW: 6A23127 CRC32:
 Query Match 8.5% Score 13: DB 11: Length 111:
 Best Local Similarity 100.0% Pred. No. 5.13e-15:
 Matches 13: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 DB 17 SYNSCASGTT 29
 QY 36 SYNSCASGTT 48
 RESULT 6
 ID 070568 PRELIMINARY: PRT: 121 AA.
 AC 070568: (REMBL: 07, CREATED)
 DT 01-AUG-1998 (REMBL: 07, LAST SEQUENCE UPDATE)
 DT 01-AUG-1998 (REMBL: 07, LAST ANNOTATION UPDATE)
 DE SINGLE CHAIN TV (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUTHERIA: RODENTIA.
 OC EUTHERIA: RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 97058313.
 RA KIMURA H., YOSHIMURA H., TANAKA K., SATOHARA T., KASAI F., ITOI S.,
 DR EMBL: D87081, G1565186.
 DR PFM: PFM0047, 19.
 FT SIGNAL 1 19
 FT CHAIN 20 >138
 SQ SEQUENCE 138 AA: 15648 MW: 7350DD0A CRC32:
 Query Match 9.2% Score 14: DB 11: Length 138:
 Best Local Similarity 100.0% Pred. No. 1.10e-17:
 Matches 14: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RA BATESCH H., KOLA A., KLOS A., KOSCH T.
RL SUBMITTED (OCT-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR EMBL: AJ225590; E1287529; -.
KW PNASID.
FT NON_TER 1 1
FT NON_TER 121 122
SQ SEQUENCE 121 AA: 13255 MW; A63C9DD CRC32: -

Query Match 8.5%; Score 13; DB 11; Length 121;
Best Local Similarity 100.0%; Pred. No. 5.1e-15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 108 DPMOCTSYTSS 120
QY 125 DPMOCTSYTSS 137
|||||

RESULT 7 PRELIMINARY; PRT: 152 AA.

ID 061552
AC 061552
DT 01-NOV-1996 (TRENDAEL, 01, CREATED)
DT 01-NOV-1996 (TRENDAEL, 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TRENDAEL, 06, LAST ANNOTATION UPDATE)
DE ANTI-HV-1 REVERSE TRANSCRIPTASE PRECURSOR.

OC EUTHERIA: RODENTIA.
OC EUTHERIA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN 11 SEQUENCE FROM N.A.
RC STRAIN: BALB/C;
RX MEDLINE: 96114009.
RA THIRION S., MONTANIS R., HETZIGEN H., RAUS J., VANDEVYVER C.;
RL IMMUNOGENETICS 43:167-168(1996).
DR PNAS: P00047; 15.
KW SIGNAL.

FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 152 ANTI-HV-1 B-CELL RECEPTOR.
SQ SEQUENCE 152 AA: 16317 MW; A63E9253 CRC32: -

Query Match 8.5%; Score 13; DB 11; Length 152;
Best Local Similarity 100.0%; Pred. No. 5.1e-15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 34 GASTRINSCASCT 46
QY 34 GASTRINSCASCT 46
|||||

RESULT 8 PRELIMINARY; PRT: 262 AA.

Query Match 7.8%; Score 12; DB 11; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.9e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 104 SLTSDSNAVTC 115
QY 104 SLTSDSNAVTC 115
|||||

RESULT 10 PRELIMINARY; PRT: 243 AA.

ID 051140
AC 051140
DT 01-JAN-1998 (TRENDAEL, 05, CREATED)
DT 01-JAN-1998 (TRENDAEL, 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TRENDAEL, 07, LAST ANNOTATION UPDATE)
DE MUS MUSCULUS (MOUSE).

OC EUTHERIA: RODENTIA.
OC EUTHERIA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN 11 SEQUENCE FROM N.A.
RC STRAIN: BALB/C;
RX MEDLINE: 96114009.
RA KLINER A., BARTH S., MATTHEI B., LEMKE H., ARENDT J.W., DIEHL V.,
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR PNAS: P00047; 15.
KW SIGNAL.

FT NON_TER 243 243
SQ SEQUENCE 243 AA: 26225 MW; E0AD5183 CRC32: -

Query Match 7.2%; Score 11; DB 11; Length 243;
Best Local Similarity 100.0%; Pred. No. 6.97e-10;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 16 VMSCHASCT 28
QY 37 VMSCHASCT 47
|||||

RESULT 11 PRELIMINARY; PRT: 37 AA.

ID 053114
AC 053114
DT 01-JUN-1998 (TRENDAEL, 06, CREATED)
DT 01-JUN-1998 (TRENDAEL, 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TRENDAEL, 06, LAST ANNOTATION UPDATE)
DE E3 ANTI-14-HYDROXY-3-NITROPHENYL(PHENOLATE + PHENOLIC FORM) ACETYL
MAB V-H REGION (FRAGMENT).
OC EUTHERIA: RODENTIA.
OC EUTHERIA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN 11 SEQUENCE FROM N.A.
RC STRAIN: BALB/C;
RX MEDLINE: 96114009.
RA KLINER A., BARTH S., MATTHEI B., LEMKE H., ARENDT J.W., DIEHL V.,
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR PNAS: P00047; 15.
KW SIGNAL.

AC 031842
DT 01-JAN-1998 (TRENDAEL, 05, CREATED)
DT 01-JAN-1998 (TRENDAEL, 05, LAST SEQUENCE UPDATE)
DT 01-AUG-1998 (TRENDAEL, 07, LAST ANNOTATION UPDATE)
DE ANTI-HV-1 REVERSE TRANSCRIPTASE SINGLE-CHAIN VARIABLE FRAGMENT.
OC EUTHERIA: RODENTIA.
OC EUTHERIA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN 11 SEQUENCE FROM N.A.
RC STRAIN: BALB/C;
RX MEDLINE: 96114009.
RA SHANER F., DUN L., ENO M., BAGASIA O., POMERANTZ R.J.;
RL J. VIROL. 70:1392-1400(1996).
DR PNAS: P00047; 15.
KW SIGNAL.

Query Match 8.5%; Score 13; DB 11; Length 262;
Best Local Similarity 100.0%; Pred. No. 5.1e-15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 250 DPMOCTSYTSS 262
QY 125 DPMOCTSYTSS 137
|||||

RESULT 9 PRELIMINARY; PRT: 134 AA.

ID 061552
AC 061552
DT 01-NOV-1996 (TRENDAEL, 01, CREATED)
DT 01-NOV-1996 (TRENDAEL, 01, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TRENDAEL, 06, LAST ANNOTATION UPDATE)
DE ANTI-HV-1 REVERSE TRANSCRIPTASE PRECURSOR.

OC EUTHERIA: RODENTIA.
OC EUTHERIA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN 11 SEQUENCE FROM N.A.
RC STRAIN: BALB/C;
RX MEDLINE: 96114009.
RA THIRION S., MONTANIS R., HETZIGEN H., RAUS J., VANDEVYVER C.;
RL IMMUNOGENETICS 43:167-168(1996).
DR PNAS: P00047; 15.
KW SIGNAL.

FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 152 ANTI-HV-1 B-CELL RECEPTOR.
SQ SEQUENCE 152 AA: 16317 MW; A63E9253 CRC32: -

Query Match 8.5%; Score 13; DB 11; Length 262;
Best Local Similarity 100.0%; Pred. No. 5.1e-15;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 34 GASTRINSCASCT 46
QY 34 GASTRINSCASCT 46
|||||

Query Match 6.5%; Score 10; DB 11; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.9e-07;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 26 SLTSDSNAVTC 33
QY 104 SLTSDSNAVTC 115
|||||

RESULT 12 PRELIMINARY; PRT: 98 AA.

ID 051113
AC 051113
DT 01-JUN-1998 (TRENDAEL, 06, CREATED)
DT 01-JUN-1998 (TRENDAEL, 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TRENDAEL, 06, LAST ANNOTATION UPDATE)
DE E3 ANTI-14-HYDROXY-3-NITROPHENYL(PHENOLATE + PHENOLIC FORM) ACETYL MAB V-H
REGION (FRAGMENT).
OC EUTHERIA: RODENTIA.
OC EUTHERIA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN 11 SEQUENCE FROM N.A.
RC STRAIN: BALB/C;
RX MEDLINE: 96114009.
RA KLINER A., BARTH S., MATTHEI B., LEMKE H., ARENDT J.W., DIEHL V.,
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR PNAS: P00047; 15.
KW SIGNAL.

FT NON_TER 98 98
SQ SEQUENCE 98 AA: 10865 MW; A631A89 CRC32: -

Query Match 6.5%; Score 10; DB 11; Length 98;
Best Local Similarity 90.9%; Pred. No. 1.92e-07;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 84 SELSDSNAVTC 94
QY 103 SELSDSNAVTC 113
|||||

RESULT 13 PRELIMINARY; PRT: 98 AA.

ID 053114
AC 053114
DT 01-JUN-1998 (TRENDAEL, 06, CREATED)
DT 01-JUN-1998 (TRENDAEL, 06, LAST SEQUENCE UPDATE)
DT 01-JUN-1998 (TRENDAEL, 06, LAST ANNOTATION UPDATE)
DE E3 ANTI-14-HYDROXY-3-NITROPHENYL(PHENOLATE + PHENOLIC FORM) ACETYL
MAB V-H REGION (FRAGMENT).
OC EUTHERIA: RODENTIA.
OC EUTHERIA: CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN 11 SEQUENCE FROM N.A.
RC STRAIN: BALB/C;
RX MEDLINE: 96114009.
RA KLINER A., BARTH S., MATTHEI B., LEMKE H., ARENDT J.W., DIEHL V.,
RL SUBMITTED (MAY-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
DR PNAS: P00047; 15.
KW SIGNAL.

MOI: INTRONL 0.0-0.1997)
 DR EMBL: AF035786; G2655850;
 FT NON_TER 1
 FT NON_TER 98
 SQ SEQUENCE 98 AA: 10912 MW: 4890186 CRC32: ---
 Query Match 5.2%: Score 8; DB 4; Length 98;
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;
 Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 SCANSCT 28
 OY 40 SCANSCT 47
 RESULT 20
 ID C99824 PRELIMINARY: PRT: 124 AA.
 AC C99824 (PRELIMINARY: 03, CREATED)
 DT 01-MAY-1997 (TRIMBLABEL: 03, LAST SEQUENCE UPDATE)
 DE 01-JUN-1998 (TRIMBLABEL: 06, LAST ANNOTATION UPDATE)
 DE ANTI-HIV-1 GP120 ANTIBODY P35 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 OS HOMO SAPIENS (HUMAN).
 OC EUTHERIA: PRIMATES.
 RN 111
 RP SEQUENCE FROM N.A.
 RC TISSUE-BONE-MARROW; P.M.H.I., BINKLEY J.M., SODROSKI J., MOORE J.P.,
 BA BARNES C.P., BURTON D.B.,
 DR EMBL: D82771; G1785876;
 DR PPM: P00047; 19. 124
 SQ SEQUENCE 124 AA: 13450 MW: 8713000 CRC32: ---

Query Match 5.2%: Score 8; DB 4; Length 124;
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;
 Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 106 LDYMOCT 113
 OY 124 LDYMOCT 111
 RESULT 21
 ID C99846 PRELIMINARY: PRT: 125 AA.
 AC C99846 (PRELIMINARY: 03, CREATED)
 DT 01-MAY-1997 (TRIMBLABEL: 03, LAST SEQUENCE UPDATE)
 DE 01-MAY-1997 (TRIMBLABEL: 03, LAST SEQUENCE UPDATE)
 DE 01-JUN-1998 (TRIMBLABEL: 06, LAST ANNOTATION UPDATE)

PT CHAIN 20 >112 POTENTIAL.
 FT NON_TER 112
 SQ SEQUENCE 112 AA: 14674 MW: 9364000 CRC32: ---
 Query Match 5.2%: Score 8; DB 7; Length 112;
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;
 Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 103 DSATVCA 110
 OY 109 DSATVCA 116
 RESULT 23
 ID P97771 PRELIMINARY: PRT: 241 AA.
 AC P97771 (PRELIMINARY: 03, CREATED)
 DT 01-MAY-1997 (TRIMBLABEL: 03, LAST SEQUENCE UPDATE)
 DE 01-MAY-1997 (TRIMBLABEL: 03, LAST SEQUENCE UPDATE)
 DE 01-JUN-1998 (TRIMBLABEL: 06, LAST ANNOTATION UPDATE)
 DE ANTI-CD47 SINGLE CHAIN PV FRAGMENT (FRAGMENT).
 OS EUTHERIA: RODENTIA.
 OC EUTHERIA: RODENTIA.
 RN 111
 RP SEQUENCE FROM N.A.
 RC KIM I.J., CHOI I.H., CHUNG H.K.,
 RA KIM I.J., CHOI I.H., CHUNG H.K.,
 DR EMBL: U88087; G1850548;
 DR PPM: P00047; 19. 1
 FT NON_TER 241
 SQ SEQUENCE 241 AA: 26086 MW: 8882020 CRC32: ---

Query Match 5.2%: Score 8; DB 11; Length 241;
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;
 Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 SCANSCT 28
 OY 40 SCANSCT 47
 RESULT 24
 ID P000288 PRELIMINARY: PRT: 244 AA.
 AC P000288 (PRELIMINARY: 04, CREATED)
 DT 01-JUL-1997 (TRIMBLABEL: 04, LAST SEQUENCE UPDATE)
 DE 01-JUL-1997 (TRIMBLABEL: 04, LAST SEQUENCE UPDATE)
 DE 01-JUL-1997 (TRIMBLABEL: 04, LAST SEQUENCE UPDATE)
 DE SINGLE CHAIN PV FRAGMENT (FRAGMENT).
 GN SCVP

DE PLATELET MEMBRANE GLYCOPROTEIN IB (CD1B) SPECIFIC ANTIBODY (FRAGMENT).
 GN V1-02
 OS HOMO SAPIENS (HUMAN).
 OC EUTHERIA: PRIMATES.
 OC EUTHERIA: PRIMATES.
 RN 111
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 91370554;
 RA HIRATA A., NIGEM D.J., MILLER E.C.;
 DR EMBL: U00411; E339711;
 DR PPM: P00047; 19. 1
 FT NON_TER 125
 SQ SEQUENCE 125 AA: 13722 MW: 8578254 CRC32: ---

Query Match 5.2%: Score 8; DB 4; Length 125;
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;
 Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 SCANSCT 28
 OY 40 SCANSCT 47
 RESULT 22
 ID C01177 PRELIMINARY: PRT: 132 AA.
 AC C01177 (PRELIMINARY: 01, CREATED)
 DT 01-NOV-1996 (TRIMBLABEL: 01, LAST SEQUENCE UPDATE)
 DE 01-NOV-1996 (TRIMBLABEL: 01, LAST SEQUENCE UPDATE)
 DE 01-JUN-1998 (TRIMBLABEL: 06, LAST ANNOTATION UPDATE)
 DE HRC CLASS II I-4-ALPHA mRNA
 DE (H-2B). 5' END. HYBRIDOMA AF.3.C7 PRECURSOR (FRAGMENT).
 OS MUS MUSCULUS (MOUSE).
 OC EUTHERIA: RODENTIA.
 RN 111
 RP SEQUENCE FROM N.A.
 RC J. HONIGEL, 198 3991-3995 (1987).
 RA CHOU H.S., WHITLEY P.J., TAPP J.A., PIERCE C.W., SIEVACH E.M.,
 DR EMBL: U15188; G194600;
 DR PPM: P00047; 19. 1
 FT SIGNAL 1 19 POTENTIAL.

OS HOMO SAPIENS (HUMAN).
 OC EUTHERIA: PRIMATES.
 OC EUTHERIA: PRIMATES.
 RN 111
 RP SEQUENCE FROM N.A.
 RC ROYERMAN R.E., WING M.G., WINTER C.;
 DR EMBL: U10571; E112725;
 DR PPM: P00047; 19. 1
 FT NON_TER 244
 SQ SEQUENCE 244 AA: 26127 MW: 8671488 CRC32: ---

Query Match 5.2%: Score 8; DB 4; Length 244;
 Best Local Similarity 100.0%; Pred. No. 6.54e-03;
 Matches 8: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 21 SCANSCT 28
 OY 40 SCANSCT 47
 RESULT 25
 ID C01224 PRELIMINARY: PRT: 38 AA.
 AC C01224 (PRELIMINARY: 05, CREATED)
 DT 01-JUN-1998 (TRIMBLABEL: 05, LAST SEQUENCE UPDATE)
 DE 01-JUN-1998 (TRIMBLABEL: 05, LAST SEQUENCE UPDATE)
 DE 01-AUG-1998 (TRIMBLABEL: 07, LAST ANNOTATION UPDATE)
 DE CD33-IG (FRAGMENT).
 OS HOMO SAPIENS (HUMAN).
 OC EUTHERIA: PRIMATES.
 RN 111
 RP SEQUENCE FROM N.A.
 RC OTTENBIELE C.H., STEVENSON F.K.;
 RA OTTENBIELE C.H., STEVENSON F.K.;
 DR EMBL: A000411; E339711;
 DR PPM: P00047; 19. 1
 FT NON_TER 38
 SQ SEQUENCE 38 AA: 4355 MW: 3788917 CRC32: ---

Query Match 4.8%: Score 7; DB 4; Length 38;
 Best Local Similarity 100.0%; Pred. No. 7.35e-03;
 Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 01-MAY-1997 (TREMBL, 03, CREATED)
 DT 01-MAY-1997 (TREMBL, 03, LAST SEQUENCE UPDATE)
 DT 01-JUN-1998 (TREMBL, 05, LAST ANNOTATION UPDATE)
 DE ANT-HIV-1 GP120 ANTIBODY P7 HEAVY CHAIN VARIABLE REGION (FRAGMENT)
 OS HOMO SAPIENS (HUMAN)
 OC CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA
 RN [1]
 RP SEQUENCE FROM N.A.
 RC B. D. BORTON, P. M. H. I., D. L. J. M., SODROSKI J., MOORE J.P.,
 RA BARBAS C.P., BORTON D.R.;
 RL SUBMITTED (DEC-1996) TO ENGL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 082767; GI785681;
 RN PRN: P00047; 19;
 PT NON-TER
 SO SEQUENCE 136 AA: 14644 MW; 3604ADIA CRC32;
 Query Match 4.64; Score 7; DB 4; Length 136;
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 39 PROCLIN 45
 QY 60 PROCLIN 66
 RESULT 34
 ID 0103060
 AC 031060;
 DT 01-JAN-1998 (TREMBL, 05, CREATED)
 DT 01-JAN-1998 (TREMBL, 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBL, 05, LAST ANNOTATION UPDATE)
 DE HYPHOSIN, 15.9 KD PROTEIN.
 OS MYCOBACTERIUM LEPRAE.
 OC PROKARYOTA: BACTERIA: ACTINOMYCETES: MYCOBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC B. D. BORTON, P. M. H. I., D. L. J. M., SODROSKI J., MOORE J.P.,
 RA BARBAS C.P., BORTON D.R.;
 RL SUBMITTED (SEP-1997) TO ENGL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 082767; GI785681;
 RN PRN: P00047; 19;
 PT NON-TER
 SO SEQUENCE 136 AA: 14644 MW; 3604ADIA CRC32;
 Query Match 4.64; Score 7; DB 4; Length 136;
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 39 PROCLIN 45
 QY 60 PROCLIN 66
 RESULT 34
 ID 0103060
 AC 031060;
 DT 01-JAN-1998 (TREMBL, 05, CREATED)
 DT 01-JAN-1998 (TREMBL, 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBL, 05, LAST ANNOTATION UPDATE)
 DE HYPHOSIN, 15.9 KD PROTEIN.
 OS MYCOBACTERIUM LEPRAE.
 OC PROKARYOTA: BACTERIA: ACTINOMYCETES: MYCOBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC B. D. BORTON, P. M. H. I., D. L. J. M., SODROSKI J., MOORE J.P.,
 RA BARBAS C.P., BORTON D.R.;
 RL SUBMITTED (SEP-1997) TO ENGL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 082767; GI785681;
 RN PRN: P00047; 19;
 PT NON-TER
 SO SEQUENCE 136 AA: 14644 MW; 3604ADIA CRC32;
 Query Match 4.64; Score 7; DB 4; Length 136;
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE (FRAGMENT).
 OS MYCOBACTERIUM LEPRAE.
 OC PROKARYOTA: BACTERIA: ACTINOMYCETES: MYCOBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC B. D. BORTON, P. M. H. I., D. L. J. M., SODROSKI J., MOORE J.P.,
 RA BARBAS C.P., BORTON D.R.;
 RL SUBMITTED (SEP-1997) TO ENGL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 082767; GI785681;
 RN PRN: P00047; 19;
 PT NON-TER
 SO SEQUENCE 136 AA: 14644 MW; 3604ADIA CRC32;
 Query Match 4.64; Score 7; DB 4; Length 136;
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 39 PROCLIN 45
 QY 60 PROCLIN 66
 RESULT 34
 ID 0103060
 AC 031060;
 DT 01-JAN-1998 (TREMBL, 05, CREATED)
 DT 01-JAN-1998 (TREMBL, 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBL, 05, LAST ANNOTATION UPDATE)
 DE HYPHOSIN, 15.9 KD PROTEIN.
 OS MYCOBACTERIUM LEPRAE.
 OC PROKARYOTA: BACTERIA: ACTINOMYCETES: MYCOBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC B. D. BORTON, P. M. H. I., D. L. J. M., SODROSKI J., MOORE J.P.,
 RA BARBAS C.P., BORTON D.R.;
 RL SUBMITTED (SEP-1997) TO ENGL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 082767; GI785681;
 RN PRN: P00047; 19;
 PT NON-TER
 SO SEQUENCE 136 AA: 14644 MW; 3604ADIA CRC32;
 Query Match 4.64; Score 7; DB 4; Length 136;
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR EMBL: 082767; GI785681;
 RN PRN: P00047; 19;
 PT NON-TER
 SO SEQUENCE 136 AA: 14644 MW; 3604ADIA CRC32;
 Query Match 4.64; Score 7; DB 4; Length 136;
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 39 PROCLIN 45
 QY 60 PROCLIN 66
 RESULT 34
 ID 0103060
 AC 031060;
 DT 01-JAN-1998 (TREMBL, 05, CREATED)
 DT 01-JAN-1998 (TREMBL, 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1998 (TREMBL, 05, LAST ANNOTATION UPDATE)
 DE HYPHOSIN, 15.9 KD PROTEIN.
 OS MYCOBACTERIUM LEPRAE.
 OC PROKARYOTA: BACTERIA: ACTINOMYCETES: MYCOBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC B. D. BORTON, P. M. H. I., D. L. J. M., SODROSKI J., MOORE J.P.,
 RA BARBAS C.P., BORTON D.R.;
 RL SUBMITTED (SEP-1997) TO ENGL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 082767; GI785681;
 RN PRN: P00047; 19;
 PT NON-TER
 SO SEQUENCE 136 AA: 14644 MW; 3604ADIA CRC32;
 Query Match 4.64; Score 7; DB 4; Length 136;
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE (FRAGMENT).
 OS MYCOBACTERIUM LEPRAE.
 OC PROKARYOTA: BACTERIA: ACTINOMYCETES: MYCOBACTERIACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC B. D. BORTON, P. M. H. I., D. L. J. M., SODROSKI J., MOORE J.P.,
 RA BARBAS C.P., BORTON D.R.;
 RL SUBMITTED (SEP-1997) TO ENGL/GENBANK/DBJ DATA BANKS.
 DR EMBL: 082767; GI785681;
 RN PRN: P00047; 19;
 PT NON-TER
 SO SEQUENCE 136 AA: 14644 MW; 3604ADIA CRC32;
 Query Match 4.64; Score 7; DB 4; Length 136;
 Best Local Similarity 100.0%; Pred. No. 7.10e-01;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

08 SHIGELLA FLEXNER;
09 SCOTOBACTERIALE; SCOTOBACTERIA: FACULTATIVELY ANAEROBIC RODS;
10 ENTEROBACTERIALE;
11 ]
12 SEQUENCE FROM N.A.
13 RX MEDLINE+SH6200316
14 ROBERTS M., REVIEWS P.R.;
15 MOL. MICROBIOL. 12:855-856(1994).
16 ]
17 SEQUENCE FROM N.A.
18 STRAIN=SH6200.
19 MEDLINE+SH6200.
20 RAVANNAVAR K., JOSE B.H., SAGANAMA C., OKADA N., YOSHITAKA N.,
21 RL J. BACTERIOL. 176:235-237(1994).
22 * SEQUENCE 289 AA; 33565 MW; 95651EED CRC32;
23 Query Match 4.8% Score 7, DB 2, Length 289,
24 Best Local Similarity 100.0%, Positives 7, Gaps 0
25 Matches 7, Conservative 0, Mismatches 0, Indels 0, Gaps 0
26 QY 71 PROBEQT 77

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BA PRIBIELA, J., BARNES C.T., CHEN J., CHURCH D., BUCKLEY A., BAIRDPALE S.
 RA MCDONALD N.M., REMARK H.R., GUSTILA W.H., DUVOI M.P., AMBROSE C.M.,
 DR SUBMITTED (JUN-1988) TO EMBL/GEMBL/DDBJ DATA BANKS.
 CR EMBL AF064964; G3792356;
 PT NON-TERMINAL PROTEIN.
 SQ SEQUENCE 604 AA: 5P5DICDA CRM32:
 Query Match 4.5% Seq No. DB 4, Length 604;
 Beat Local Similarity 100.0% Prid No. 7, 10-0;
 Matches 7: Conservative 0: Indels 0: Gaps 0
 Mismatches 0: Indels 0: Gaps 0
 Oy 102 15817582 108

[illegible]

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Query Match: 4.68; Score 7; DB 5; Length 998;
Best Local Similarity 100.00; Pred. No. 7.10e-01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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	Query Match	4.6%	Score 7:	DB 2:	Length 322:
	Best Local Similarity	100.0%:	Pred. No.	7.10e-01:	
	Matches	7:	Conservative	0:	Mismatches 0; Indels 0;
Db	299 LSITTCV 305				Gaps 0
CY	LSITTCV 17				

RESULT	41	
ID	069789	PRELIMINARY;
AC	069789;	PRT; 399 AA

BT	01-AUG-1998	07, (CREATED)
DT	01-AUG-1998	07, LAST SEQUENCE UPDATE)
DT	01-AUG-1998	07, LAST SEQUENCE UPDATE)
DE	INDOLE DIOXYGENASE.	
GN	BPEA.	

03 RHODOCOCUS OPACUS.
0C EUBACTERIA: FIRMICUTES; ACTINOMYCETES; NOCARDIOFORM ACTINOMYCETES,
0C RHODOCOCUS.

RP SEQUENCE FROM N.A.
RC STRAIN=NCIB12038;
RA KULAKOV L.A., LARKIN M.J.;

DR EMBL; AJ005688; E1288484; -
KM DIOXYGENASE.
SO SEQUENCE 399 AA; 43151 MW; D3013412 STR37

Query Match	4.6%	Score 7;	DB 2;	Length 399
Best Local Similarity	100.0%	Pred. No.	7.10e-01;	
Matches	7			

Db	230	GDYYNQ	236
QY	75	GDYYNQ	81

RESULT	42		
ID	043606	PRELIMINARY;	PRT; 604 AA
AC	043606;		

DT	01-JUN-1998	(TREMBLREL. 06, CREATED)
DT	01-JUN-1998	(TREMBLREL. 06, LAST SEQUENCE UPDATE)
DT	01-AUG-1998	(TREMBLREL. 07, LAST ANNOTATION UPDATE)
DE	HYPOTHETICAL 69.8 KD PROTEIN (P48699P)	

OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA
OC EUETHERIA; PRIMATES.
[1]

RP SEQUENCE FROM N.A.

05	001202	PRELIMINARY	PRI. 2157 MA.
06	001203		
07	001204	002108	002109
08	001205	002110	002111
09	001206	002112	002113
10	001207	002114	002115
11	001208	002116	002117
12	001209	002118	002119
13	001210	002120	002121
14	001211	002122	002123
15	001212	002124	002125
16	001213	002126	002127
17	001214	002128	002129
18	001215	002130	002131
19	001216	002132	002133
20	001217	002134	002135
21	001218	002136	002137
22	001219	002138	002139
23	001220	002140	002141
24	001221	002142	002143
25	001222	002144	002145
26	001223	002146	002147
27	001224	002148	002149
28	001225	002150	002151
29	001226	002152	002153
30	001227	002154	002155
31	001228	002156	002157
32	001229	002158	002159
33	001230	002160	002161
34	001231	002162	002163
35	001232	002164	002165
36	001233	002166	002167
37	001234	002168	002169
38	001235	002170	002171
39	001236	002172	002173
40	001237	002174	002175
41	001238	002176	002177
42	001239	002178	002179
43	001240	002180	002181
44	001241	002182	002183
45	001242	002184	002185
46	001243	002186	002187
47	001244	002188	002189
48	001245	002190	002191
49	001246	002192	002193
50	001247	002194	002195
51	001248	002196	002197
52	001249	002198	002199
53	001250	002200	002201
54	001251	002202	002203
55	001252	002204	002205
56	001253	002206	002207
57	001254	002208	002209
58	001255	002210	002211
59	001256	002212	002213
60	001257	002214	002215
61	001258	002216	002217
62	001259	002218	002219
63	001260	002220	002221
64	001261	002222	002223
65	001262	002224	002225
66	001263	002226	002227
67	001264	002228	002229
68	001265	002230	002231
69	001266	002232	002233
70	001267	002234	002235
71	001268	002236	002237
72	001269	002238	002239
73	001270	002240	002241
74	001271	002242	002243
75	001272	002244	002245
76	001273	002246	002247
77	001274	002248	002249
78	001275	002250	002251
79	001276	002252	002253
80	001277	002254	002255
81	001278	002256	002257
82	001279	002258	002259
83	001280	002260	002261
84	001281	002262	002263
85	001282		

RX MEDLINE; 88089537.
RA HUGHES P.J., NORTH C., TELLS C.H., MINOR P.D., STANWAY G.,
J. GEN. VIROL. 69:49-58(1988).
DE Expr. D00030. D1000000.

NAME	CHAIN	RESIDUES	VP4 PROTEIN.
PPV	1	69	
FT	70	332	
CH	71	332	
VP2	72	332	
VP3	73	332	
VP4	74	332	
VP5	75	332	
VP6	76	332	
VP7	77	332	
VP8	78	332	
VP9	79	332	
VP10	80	332	
VP11	81	332	
VP12	82	332	
VP13	83	332	
VP14	84	332	
VP15	85	332	
VP16	86	332	
VP17	87	332	
VP18	88	332	
VP19	89	332	
VP20	90	332	
VP21	91	332	
VP22	92	332	
VP23	93	332	
VP24	94	332	
VP25	95	332	
VP26	96	332	
VP27	97	332	
VP28	98	332	
VP29	99	332	
VP30	100	332	
VP31	101	332	
VP32	102	332	
VP33	103	332	
VP34	104	332	
VP35	105	332	
VP36	106	332	
VP37	107	332	
VP38	108	332	
VP39	109	332	
VP40	110	332	
VP41	111	332	
VP42	112	332	
VP43	113	332	
VP44	114	332	
VP45	115	332	
VP46	116	332	
VP47	117	332	
VP48	118	332	
VP49	119	332	
VP50	120	332	
VP51	121	332	
VP52	122	332	
VP53	123	332	
VP54	124	332	
VP55	125	332	
VP56	126	332	
VP57	127	332	
VP58	128	332	
VP59	129	332	
VP60	130	332	
VP61	131	332	
VP62	132	332	
VP63	133	332	
VP64	134	332	
VP65	135	332	
VP66	136	332	
VP67	137	332	
VP68	138	332	
VP69	139	332	
VP70	140	332	
VP71	141	332	
VP72	142	332	
VP73	143	332	
VP74	144	332	
VP75	145	332	
VP76	146	332	
VP77	147	332	
VP78	148	332	
VP79	149	332	
VP80	150	332	
VP81	151	332	
VP82	152	332	
VP83	153	332	
VP84	154	332	
VP85	155	332	
VP86	156	332	
VP87	157	332	
VP88	158	332	
VP89	159	332	
VP90	160	332	
VP91	161	332	
VP92	162	332	
VP93	163	332	
VP94	164	332	
VP95	165	332	
VP96	166	332	
VP97	167	332	
VP98	168	332	
VP99	169	332	
VP100	170	332	
VP101	171	332	
VP102	172	332	
VP103	173	33	

PT	CHAIN	571	857	VP1 PROTEIN.
PT	CHAIN	858	999	P2-A PROTEIN.
PT	CHAIN	1000	1094	P2-B PROTEIN.
PT	CHAIN	1000		

FT	CHAIN	1417	1493	P3-C PROTEIN
FT	CHAIN	1494	1514	P3-A PROTEIN
FT	CHAIN	1515	1697	VPG PROTEIN.
				PROTEASE.

Query Match	Score	DB
4.6%;	Score 7;	DB 1

Db 1111 GLEMIGN 1117
 near local similarity 100.0%; Pred. No. 7.10
 Matches 7; Conservative 0; Mismatches

QY 63 CLEMIGN 69

RESULT	45	
ID	055225	PRELIMINARY;
AC	055225;	PRT: 2910 A
DT	01-JUN-1998 (TREFMARI:PT	06
		CORRECTED

DT	01-JUN-1998	(TREMBLREL.	06,	LAST SEQUENCE
DT	01-AUG-1998	(TREMBLREL.	07,	LAST ANNOTATIO
DE	OTOGELIN.			

MS MESCHUS (MUSCULUS)
OC EUMAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 9807072.
RA COHEN-SALUDON M.; EL-AMRADI A.; LEBOVICI M.; PETIT C.;
DR PROC. NATL. ACAD. SCI. U.S.A. 94:1450-1455(1997).
SQ SEQUENCE: 2910 AA; 313410 MW; 94F5C6E8 CRC32;
Query Match 4.6%; Score 7; DB 11; Length 2910;
Best Local Similarity 100.0%; Pred. No. 7.1e+01;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 676 PLVPGSL 682
QY 147 PLVPGSL 153
RESULT 46
ID P78465 PRELIMINARY: PRT: 12 AA.
AC G01054;
DT 01-NOV-1997 (TREMBL:03, CREATED)
DT 01-NOV-1997 (TREMBL:03, LAST SEQUENCE UPDATE)
DE POLYCLONAL LAMPROM T(14:18) CHROMOSOMAL TRANSLOCATION JUNCTION.
OC EUMAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 9807072.
RA COHEN-SALUDON M.; EL-AMRADI A.; LEBOVICI M.; PETIT C.;
DR PROC. NATL. ACAD. SCI. U.S.A. 94:1450-1455(1997).
SQ SEQUENCE: 12 AA; 1297 MW; 1993DA44 CRC32;
Query Match 3.9%; Score 6; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 YNCOGT 6
QY 126 YNCOGT 131
RESULT 47
ID Q78986 PRELIMINARY: PRT: 28 AA.
AC Q78986;
DT 01-NOV-1996 (TREMBL:01, CREATED)
DT 01-NOV-1996 (TREMBL:01, LAST SEQUENCE UPDATE)
DE ECTOPARASITIC VARIOUS TYPE 1 (REV-1).
OC EUMAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 9205212.
RA LERNER R.A.; BARONAS C.F. III; PERSSON M.A.; KOENIG S.; CHANOCK R.M.;
DR PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
SQ SEQUENCE: 28 AA; 3226 MW; AE586005 CRC32;
Query Match 3.9%; Score 6; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.1e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 23 DYNQCG 28
QY 125 DYNQCG 130

DB 7 FLPLLS 12
QY 7 FLPLLS 12
RESULT 49
ID Q18715 PRELIMINARY: PRT: 56 AA.
AC Q18715;
DT 01-NOV-1998 (TREMBL:05, CREATED)
DT 01-NOV-1998 (TREMBL:05, LAST SEQUENCE UPDATE)
DE CYSTEINE PROTEASE (FRAGMENT).
OC ECTOPARASITIC VARIOUS TYPE 1 (REV-1).
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 9205212.
RA LERNER R.A.; BARONAS C.F. III; PERSSON M.A.; KOENIG S.; CHANOCK R.M.;
DR PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
SQ SEQUENCE: 56 AA; 6341 MW; D218FC87 CRC32;
Query Match 3.9%; Score 6; DB 5; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.7e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 21 NQFPG 26
QY 80 NQFPG 85
RESULT 50
ID Q41401 PRELIMINARY: PRT: 64 AA.
AC Q41401;
DT 01-NOV-1996 (TREMBL:01, CREATED)
DT 01-NOV-1996 (TREMBL:01, LAST SEQUENCE UPDATE)
DE EARLY MODULIN (EMOD-3A) PROTEIN (FRAGMENT).
OC ECTOPARASITIC VARIOUS TYPE 1 (REV-1).
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 9205212.
RA LERNER R.A.; BARONAS C.F. III; PERSSON M.A.; KOENIG S.; CHANOCK R.M.;
DR PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
SQ SEQUENCE: 64 AA; 7356 MW; 3F21DD9C CRC32;
Query Match 3.9%; Score 6; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 4.7e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 3 PPVYP 8
QY 142 PPVYP 147
Search completed: Thu Apr 15 18:10:46 1999
Job time: 77 sec.

DT 01-NOV-1996 (TREMBL:01, CREATED)
DT 01-NOV-1996 (TREMBL:01, LAST SEQUENCE UPDATE)
DE HEAVY-CHAIN COMPLEMENT-DETERMINING REGION 3 mRNA
OC ECTOPARASITIC VARIOUS TYPE 1 (REV-1).
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 9205212.
RA LERNER R.A.; BARONAS C.F. III; PERSSON M.A.; KOENIG S.; CHANOCK R.M.;
DR PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
SQ SEQUENCE: 28 AA; 3226 MW; AE586005 CRC32;
Query Match 3.9%; Score 6; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.1e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 23 DYNQCG 28
QY 125 DYNQCG 130
RESULT 48
ID Q01054 PRELIMINARY: PRT: 54 AA.
AC G01054;
DT 01-NOV-1996 (TREMBL:01, CREATED)
DT 01-NOV-1996 (TREMBL:01, LAST SEQUENCE UPDATE)
DE POLYCLONAL LAMPROM T(14:18) CHROMOSOMAL TRANSLOCATION JUNCTION.
OC EUMAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 9205212.
RA LERNER R.A.; BARONAS C.F. III; PERSSON M.A.; KOENIG S.; CHANOCK R.M.;
DR PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
SQ SEQUENCE: 54 AA; 6435 MW; B85E599C CRC32;
Query Match 3.9%; Score 6; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 4.7e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 YNCOGT 6
QY 126 YNCOGT 131

DT 01-NOV-1996 (TREMBL:01, CREATED)
DT 01-NOV-1996 (TREMBL:01, LAST SEQUENCE UPDATE)
DE HEAVY-CHAIN COMPLEMENT-DETERMINING REGION 3 mRNA
OC ECTOPARASITIC VARIOUS TYPE 1 (REV-1).
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 9205212.
RA LERNER R.A.; BARONAS C.F. III; PERSSON M.A.; KOENIG S.; CHANOCK R.M.;
DR PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
SQ SEQUENCE: 28 AA; 3226 MW; AE586005 CRC32;
Query Match 3.9%; Score 6; DB 14; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.1e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 23 DYNQCG 28
QY 125 DYNQCG 130
RESULT 48
ID Q01054 PRELIMINARY: PRT: 54 AA.
AC G01054;
DT 01-NOV-1996 (TREMBL:01, CREATED)
DT 01-NOV-1996 (TREMBL:01, LAST SEQUENCE UPDATE)
DE POLYCLONAL LAMPROM T(14:18) CHROMOSOMAL TRANSLOCATION JUNCTION.
OC EUMAROTIA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 9205212.
RA LERNER R.A.; BARONAS C.F. III; PERSSON M.A.; KOENIG S.; CHANOCK R.M.;
DR PROC. NATL. ACAD. SCI. U.S.A. 88:10134-10137(1991).
SQ SEQUENCE: 54 AA; 6435 MW; B85E599C CRC32;
Query Match 3.9%; Score 6; DB 3; Length 54;
Best Local Similarity 100.0%; Pred. No. 4.7e+01;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 YNCOGT 6
QY 126 YNCOGT 131

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972	6	4.1	860	2	14839	transferrin X - mouse (T)	1.44e+02
971	6	4.1	860	2	JCS986	A-X lines anchoring pr	1.44e+02
970	6	4.1	865	2	86904	hypothetical protein	1.44e+02
969	6	4.1	865	2	86904	hypothetical protein	1.44e+02
968	6	4.1	874	2	870041	proteobactinase - P	1.44e+02
967	6	4.1	874	2	870041	proteobactinase - P	1.44e+02
966	6	4.1	887	2	889777	hypothetical protein	1.44e+02
965	6	4.1	887	2	889777	hypothetical protein	1.44e+02
964	6	4.1	900	2	907838	SRG15 protein - yeast	1.44e+02
963	6	4.1	910	2	907838	SRG15 protein - yeast	1.44e+02
962	6	4.1	911	2	87058	ocin protein - Vibrio	1.44e+02
961	6	4.1	911	2	87058	ocin protein - Vibrio	1.44e+02
960	6	4.1	912	2	JC2125	proteobactinase - P	1.44e+02
959	6	4.1	912	2	JC2125	proteobactinase - P	1.44e+02
958	6	4.1	935	2	135942	zees8 - rat (transmem	1.44e+02
957	6	4.1	935	2	135942	zees8 - rat (transmem	1.44e+02
956	6	4.1	1064	2	841342	adenylate cyclase (EC	1.44e+02
955	6	4.1	1064	2	841342	adenylate cyclase (EC	1.44e+02
954	6	4.1	1155	2	863932	PEAT protein - yeast	1.44e+02
953	6	4.1	1155	2	863932	PEAT protein - yeast	1.44e+02
952	6	4.1	1155	2	871458	Vacuolar protein Vac7	1.44e+02
951	6	4.1	1155	2	871458	Vacuolar protein Vac7	1.44e+02
950	6	4.1	1266	2	861200	hypothetical nucleoside re	1.44e+02
949	6	4.1	1266	2	861200	hypothetical nucleoside re	1.44e+02
948	6	4.1	1343	2	135164	hypothetical protein	1.44e+02
947	6	4.1	1343	2	135164	hypothetical protein	1.44e+02
946	6	4.1	1352	2	A35233	kinase-related transp	1.44e+02
945	6	4.1	1352	2	A35233	kinase-related transp	1.44e+02
944	6	4.1	1897	1	TDWU1	lambocyte antigen-eta	1.44e+02
943	6	4.1	1897	1	TDWU1	lambocyte antigen-eta	1.44e+02
942	6	4.1	1968	2	871161	probable integrin, mem	1.44e+02
941	6	4.1	1968	2	871161	probable integrin, mem	1.44e+02
940	6	4.1	2090	2	828058	probable transmembran	1.44e+02
939	6	4.1	2090	2	828058	probable transmembran	1.44e+02
938	6	4.1	2228	2	81285V	genomic polyprotein -	1.44e+02
937	6	4.1	2228	2	81285V	genomic polyprotein -	1.44e+02
936	6	4.1	2444	2	CA1400	calcium channel, Bi-2	1.44e+02
935	6	4.1	2444	2	CA1400	calcium channel, Bi-2	1.44e+02
934	6	4.1	2717	2	A31253	Diphtheria toxin subun	1.44e+02
933	6	4.1	2717	2	A31253	Diphtheria toxin subun	1.44e+02
932	6	4.1	3068	1	A44066	genomic polyprotein -	1.44e+02
931	6	4.1	3068	1	A44066	genomic polyprotein -	1.44e+02
930	6	4.1	5232	2	A45065	HC-toxin synthetase -	1.44e+02

[illegible]

Mon Apr 19 13:23:52 1995

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[illegible]

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CLASSIFICATION
  KERNOWS
  FORMER
  1-5
  6-16
  17-31
  32-47
  48-63
  64-79
  80-95
  96-111
  112-127
  128-143
  144-159
  160-175
  176-191
  192-207
  208-223
  224-239
  240-255
  256-271
  272-287
  288-303
  304-319
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  592-607
  608-623
  624-639
  640-655
  656-671
  672-687
  688-703
  704-719
  720-735
  736-751
  752-767
  768-783
  784-799
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  832-847
  848-863
  864-879
  880-895
  896-911
  912-927
  928-943
  944-959
  960-975
  976-991
  992-1007
  1008-1023
  1024-1039
  1040-1055
  1056-1071
  1072-1087
  1088-1103
  1104-1119
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  1136-1151
  1152-1167
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Mon Apr 19 13:23:52 1999

US-00-036-455-2.FPJ

Page 24

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 Mperch_pp protein - protein database search, using Smith-Waterman algorithm
 Date: Thu Apr 15 18:00:56 1999; Maspar time 8.71 Seconds
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Title: >US-08-836-455-4
 Description: (1-153) from US08836455.pep
 Perfect Score: 1109
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Scoring table:
 Gap 11
 PAM 150

Searched: 116695 segs, 37453910 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: plr58
 1:plr1 2:plr2 3:plr3 4:plr4

Statistics: Mean 42.120; Variance 104.479; scale 0.403
 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

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3	774	69.8	469	2 S37483	Ig gamma-2a chain - m	1.37e-104
4	767	69.2	151	2 PU0011	Ig heavy chain precu	2.00e-103
5	763	68.8	150	2 PN0444	Ig heavy chain V regi	9.21e-103
6	746	67.3	139	2 PS0024	Ig heavy chain precu	6.10e-100
7	742	66.9	166	2 PU0012	Ig heavy chain precu	2.81e-99
8	727	65.6	137	2 H32513	Ig heavy chain precu	8.57e-97
9	724	65.3	246	2 S38950	Ig gamma chain - mous	2.69e-96
10	724	65.3	446	2 S40295	Ig gamma-2a chain (m)	5.57e-94
11	710	64.0	178	2 S29594	Ig gamma chain (m65)	5.13e-94
12	709	63.9	140	1 HYMSG7	Ig heavy chain precu	8.15e-94
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28	670	60.2	135	2 PH1492	Ig heavy chain V regi	2.23e-87
29	668	60.2	140	2 PH1486	Ig heavy chain V regi	4.76e-87
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32	661	59.6	133	2 PC1155	Ig heavy chain precu	6.77e-86
33	658	59.3	140	2 A36194	Ig heavy chain V regi	2.11e-85
34	655	59.1	139	2 MHMS18	Ig heavy chain precu	6.38e-85
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ALIGNMENTS

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 ORGANISM Mus musculus #common_name mouse
 DATE 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 08-Sep-1997

ACCESSIONS
 S01321
 REFERENCE
 #authors de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
 Eur. J. Biochem. (1988) 176:287-295
 #journal Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed against the tumour marker human placental alkaline phosphatase.
 #citations 1
 #cross-references M01D:8329081
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 ##residues 1-475 #label DB1
 ##cross-references EMBL:X13186; NID:g51780; PID:g51781
 #note this sequence was determined from the differentiated

CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
 KEYWORDS immunoglobulin
 FEATURE

1-19 #domain signal sequence #status predicted #label SIG
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 DEFINITION Mouse Ig rearranged H-chain V-region mRNA VJ1.
 ACCESSION M17953
 NID g196223
 KEYWORDS C-region; V-region; immunoglobulin heavy chain; processed gene.
 SOURCE Mus musculus cDNA to mRNA.
 ORGANISM Mus musculus
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae; Murinae; Mus.
 1 (bases 1 to 458)
 Liu, A.Y., Robinson, R.R., Murray, E.D. Jr., Ledbetter, J.A., Hellstrom, I. and Hellstrom, K.E.
 Production of a mouse-human chimeric monoclonal antibody to CD20 with potent FC-dependent biological activity
 J. Immunol. 139, 3521-3526 (1987)
 MEDLINE 88060445
 COMMENT Draft entry and computer-readable sequence [1] kindly submitted by A.Y. Liu, 02-FEB-1987.
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 DEFINITION Sequence 37 from Patent EP 0274394.
 ACCESSION 105921
 NID 9590876
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 458)
 Robinson, R.R., Liu, A.Y., Hellstrom, K.E., Hellstrom, I. and Ledbetter, J.A.
 Chimeric antibody with specificity to human B cell surface antigen
 Patent: EP 0274394-A2 37 13-JUL-1988;
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RESULT 4
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 DEFINITION Sequence 12 from Patent WO 8804936.
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 NID 9588489
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 458)
 Robinson, R.R., Liu, A.Y., Hellstrom, K.E., Hellstrom, I. and Ledbetter, J.A.
 Patent: WO 8804936-A 12 14-JUL-1988;
 FEATURES
 source Location/Qualifiers
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 /organism="unknown"

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 WISE (TM)

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 on: Thu Apr 15 17:57:49 1999; Maspar time 8.66 Seconds
 627.099 Million cell updates/sec
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 Perfect Score: 1019
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Scoring table: PAM 150
 Gap 11

Searched: 116695 seqs, 37453910 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

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Statistics: Mean 42.409; Variance 104.536; scale 0.406

Prod. No. is the number of results predicted by chance to have a
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 and is derived by analysis of the total score distribution.

SUMMARIES

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26	588	57.7	125	2	S40315	Ig kappa chain - huma	2.86e-74
27	588	57.7	127	2	S40367	Ig kappa chain V-J-C	2.86e-74
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34	583	57.2	139	2	S40365	Ig kappa chain - huma	1.30e-73
35	582	57.1	126	2	S40335	Ig kappa chain V-J-C	2.77e-73
36	581	57.0	128	1	KVMS71	Ig kappa chain precur	4.04e-73
37	580	56.9	88	2	PL0261	Ig kappa chain V regl	5.89e-73
38	580	56.9	129	2	S40332	Ig kappa chain - huma	5.89e-73
39	579	56.8	128	2	S46372	Ig kappa chain variab	8.60e-73
40	578	56.7	128	2	PL0101	Ig kappa chain precur	1.25e-72
41	576	56.5	132	2	S38646	Ig kappa chain V regl	2.67e-72
42	574	56.3	101	2	B28840	Ig kappa chain V regl	5.68e-72
43	574	56.3	127	2	S11240	Ig kappa chain V regl	5.68e-72
44	573	56.2	101	2	C28840	Ig kappa chain V regl	8.29e-72
45	571	56.0	123	2	S40331	Ig kappa chain - huma	1.76e-71

ALIGNMENTS

RESULT 1

ENTRY 1
 TITLE KVMSM4 #type complete
 CONTAINS Ig kappa chain precursor V region (MORC 41) - mouse
 ORGANSIM Ig kappa chain precursor V region VK41
 ANNOTATION #formal_name Mus musculus #common_name house mouse
 DATE 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 16-Aug-1996

ACCESSIONS A93211; B93211; A93815; A94239; A01922; A01923
 A93211

REFERENCE A93211
 #authors Seidman, J.G.; Max, E.E.; Leder, P.
 #journal Nature (1979) 280:370-375
 #title A kappa-immunoglobulin gene is formed by site-specific recombination without further somatic mutation.

#cross-references MUID:79221900
 #accession A93211
 #molecule_type DNA
 #residues 1-130 #label PC41

#cross-references MUID:77148916
 #accession A93815
 #molecule_type DNA
 #residues 1-117 #label VK41

#note the sequences were determined from the differentiated gene MORC 41 and the germline gene VK41

REFERENCE A93815
 #authors Birstein, Y.; Schechter, I.
 #journal Proc. Natl. Acad. Sci. U.S.A. (1977) 74:716-720
 #title Amino acid sequence of the NH-2-terminal extra piece segments of the precursors of mouse immunoglobulin lambda-1-type and kappa-type light chains.

#cross-references MUID:67056897
 #accession A94239
 #molecule_type protein
 #residues 1-33 #label BUR

#note Met-3 is apparently used as an alternative initiator in 25% of the chains

REFERENCE A94239
 #authors Gray, W.R.; Dreyer, W.J.; Hood, L.
 #journal Science (1967) 155:465-467
 #title Mechanism of antibody synthesis: size differences between mouse kappa chains.

#cross-references MUID:67056897
 #accession A94239
 #molecule_type protein
 #residues 23-49, 'B', '51-53', '15B', '57-58', '72', '61-62', 'B2', '65-76', 'B', '78-108, 110-130 #label GRA

#experimental_source Bence Jones protein MORC 41

GENETICS #introns 19/1

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COMPLEX

An immunoglobulin heterotrimer subunit consists of two identical light (kappa or lambda) and two identical heavy (alpha, delta, epsilon, gamma, or mu) chains usually stabilized by interchain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger oligomers.

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology alternative initiators; heterotrimer; immunoglobulin

KEYWORDS 1-22

FEATURE 3-22

23-130 #domain signal sequence #status experimental #label SIG1

38-112 #product Ig kappa chain V region (MOPC 41) #status experimental #label M41

45-110 #domain immunoglobulin homology #label IMM

SUMMARY #disulfide bonds #status predicted

Query Match 82.2%; Score 838; DB 1; Length 130; Best Local Similarity 92.2%; Pred. No. 7,84e-116; Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Db 3 MRAPQIFGFLLEPGRCODIOMTOSPSLSASLGERVSLTCRASODIGSLNMLQOEP 62

Qy 1 MGAPQIIGFLLEPGRCODIOMTOSPSLSASLGERVSLTCRASODIGSLNMLQOEP 60

Db 63 DGTIRLIYATSSLDGVPKRFSGSGSDYSLTISSEDFVYICLQYATSPWTFGG 122

Qy 61 DGTIRLIYATSSLDGVPKRFSGSGSDYSLTISSEDFVYICLQYATSPWTFGG 120

Db 123 GTRKEIR 130

Qy 121 GTRKEIR 128

RESULT 2

ENTRY PLO260 #type fragment

TITLE Ig kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

ACCESSION PLO260

REFERENCE PLO231

AUTHORS Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Weigert, M.

#journal J. Exp. Med. (1990) 171:265-297

#title Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.

#cross-references MIMD:90111618

CLASSIFICATION #molecule-type mRNA

KEYWORDS #residues 1-106 #label SHL

FEATURE #superfamily immunoglobulin V region; immunoglobulin homology heterotrimer; immunoglobulin

1-23 #region framework 1\

24-34 #region complementarity-determining 1\

35-49 #region framework 2\

50-56 #region complementarity-determining 2\

57-88 #region framework 3\

89-97 #region complementarity-determining 3\

98-106 #region framework 4

SUMMARY #length 106 #checksum 2157

Query Match 67.7%; Score 690; DB 2; Length 106; Best Local Similarity 93.4%; Pred. No. 4,05e-91; Matches 99; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Db 1 D1OMTOSPSLSASLGERVSLTCRASODIGSLNMLQOEPDGTIRLIYATSSLDGVPK 60

Qy 21 D1OMTOSPSLSASLGERVSLTCRASODIGSLNMLQOEPDGTIRLIYATSSLDGVPK 80

Db 61 RFGSGRSGSDYSLTISSEDFVYICLQYATSPWTFGGGTKEI 106

Qy 81 RFGSGRSGSDYSLTISSEDFVYICLQYATSPWTFGGGTKEI 126

RESULT 3

ENTRY PLO259 #type fragment

TITLE Ig kappa chain V region (anti-DNA, DP1VK) - mouse (fragment)

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

ACCESSION PLO259

REFERENCE PLO231

AUTHORS Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.; Weigert, M.

#journal J. Exp. Med. (1990) 171:265-297

#title Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic mutation.

#cross-references MIMD:90111618

CLASSIFICATION #molecule-type mRNA

KEYWORDS #residues 1-106 #label SHL

FEATURE #superfamily immunoglobulin V region; immunoglobulin homology heterotrimer; immunoglobulin

1-23 #region framework 1\

24-34 #region complementarity-determining 1\

35-49 #region framework 2\

50-56 #region complementarity-determining 2\

57-88 #region framework 3\

89-97 #region complementarity-determining 3\

98-106 #region framework 4

SUMMARY #length 106 #checksum 2162

Query Match 67.5%; Score 688; DB 2; Length 106; Best Local Similarity 92.5%; Pred. No. 8,69e-91; Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Db 1 D1OMTOSPSLSASLGERVSLTCRASODIGSLNMLQOEPDGTIRLIYATSSLDGVPK 60

Qy 21 D1OMTOSPSLSASLGERVSLTCRASODIGSLNMLQOEPDGTIRLIYATSSLDGVPK 80

Db 61 RFGSGRSGSDYSLTISSEDFVYICLQYATSPWTFGGGTKEI 106

Qy 81 RFGSGRSGSDYSLTISSEDFVYICLQYATSPWTFGGGTKEI 126

RESULT 4

ENTRY S14237 #type complete

TITLE Ig kappa chain precursor (15C5) - mouse

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 10-Sep-1997

ACCESSION S14237

REFERENCE S14236

AUTHORS Vandamme, A.M.; Bulens, F.; Bernat, H.; Nelles, L.; Ilijen, R.H.; Collen, D.

#journal Eur. J. Biochem. (1990) 192:767-775

#title Construction and characterization of a recombinant murine monoclonal antibody directed against human fibrin fragment-D dimer.

#cross-references MIMD:91006173

CLASSIFICATION #molecule-type mRNA

KEYWORDS #residues 1-234 #label VAN

FEATURE #superfamily immunoglobulin V region; immunoglobulin heterotrimer; immunoglobulin

1-23 #region framework 1\

24-34 #region complementarity-determining 1\

35-49 #region framework 2\

50-56 #region complementarity-determining 2\

57-88 #region framework 3\

89-97 #region complementarity-determining 3\

98-106 #region framework 4

SUMMARY #length 234 #molecular-weight 26087 #checksum 6000

Query Match 67.3%; Score 686; DB 2; Length 234; Best Local Similarity 69.0%; Pred. No. 1,87e-90; Matches 98; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

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JOURNAL **structurally similar to natural autoantibodies**
Unpublished

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SOURCE      region; variable region.  
            house mouse.
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 W O R L D
 (TM)

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Search - protein - protein database search, using Smith-Waterman algorithm
 on: Tue Mar 23 15:01:25 1999; Maspar time 2.89 Seconds
 61.491 Million cell updates/sec

Tabular output not generated.

Title: >US-08-766-350A-2
 Description: (24-34) from US08766350A.pep (2 of 4)
 Perfect Score: 63
 Sequence: 1 MTQSPSSLSAS 11

Scoring table: PAM 150
 Gap 11

Searched: 131922 seqs, 16180660 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq32
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23
 24:part24 25:part25 26:part26 27:part27 28:part28
 29:part29

Statistics: Mean 15.144; Variance 52.220; scale 0.290

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	63	100.0	104	29	W52225	Antibody LD2-4-VL cha 3.52e+00
2	63	100.0	105	29	W52217	Antibody LD1-84-VL ch 3.52e+00
3	63	100.0	105	29	W52239	Antibody LD1-6-17-VL 3.52e+00
4	63	100.0	105	29	W52241	Antibody LD1-2-6-3-VL 3.52e+00
5	63	100.0	105	29	W52219	Antibody LD1-110-VL c 3.52e+00
6	63	100.0	105	29	W52237	Antibody LD2-20-VL ch 3.52e+00
7	63	100.0	105	29	W52233	Antibody LD2-14-VL ch 3.52e+00
8	63	100.0	106	29	W52213	Antibody LD1-52-VL ch 3.52e+00
9	63	100.0	106	29	W52227	Antibody LD2-5-VL cha 3.52e+00
10	63	100.0	106	29	W52221	Antibody LD1-117-VL c 3.52e+00
11	63	100.0	106	29	W52242	Humanised alpha-4 int 3.52e+00
12	63	100.0	107	29	W41390	Anti-CEA antibody 11g 3.52e+00
13	63	100.0	107	29	W41397	Anti-CEA antibody 806 3.52e+00
14	63	100.0	107	29	W23953	Chimeric humanised Mu 3.52e+00
15	63	100.0	107	29	W41413	Light chain variable 3.52e+00
16	63	100.0	107	27	W27568	Anti-TNF-alpha antibo 3.52e+00
17	63	100.0	107	21	W11920	Humanised MAb SK8-E2 3.52e+00
18	63	100.0	107	21	W11920	Humanised MAb SK8-E2 3.52e+00

Result ID	Score	Query Match	Length	ID	Description	Pred. No.
19	63	100.0	107	14	R79247	Light chain variable 3.52e+00
20	63	100.0	107	14	R78972	Light chain variable 3.52e+00
21	63	100.0	108	27	W23440	Modified light chain 3.52e+00
22	63	100.0	108	27	W23439	Modified light chain 3.52e+00
23	63	100.0	108	27	W23442	Variant variable light 3.52e+00
24	63	100.0	108	21	W04177	Light chain variable 3.52e+00
25	63	100.0	108	5	R28751	Interleukin-5 humanis 3.52e+00
26	63	100.0	113	29	W42472	Human vkap65.15 fra 3.52e+00
27	63	100.0	117	28	W41147	Humanised light chain 3.52e+00
28	63	100.0	126	28	W36164	Human/murine chimeric 3.52e+00
29	63	100.0	126	14	R76678	Human/murine chimeric 3.52e+00
30	63	100.0	126	14	R76675	Human/murine chimeric 3.52e+00
31	63	100.0	126	14	R76676	Human/murine chimeric 3.52e+00
32	63	100.0	126	14	R76680	Human/murine chimeric 3.52e+00
33	63	100.0	126	14	W04388	Humanised anti-VLA-4 3.52e+00
34	63	100.0	126	27	W31691	Humanised anti-VLA-4 3.52e+00
35	63	100.0	128	18	R90684	Humanized SC7.29 anti 3.52e+00
36	63	100.0	128	18	R90684	Humanized SC7.29 anti 3.52e+00
37	63	100.0	214	26	W34504	Light chain of human 3.52e+00
38	63	100.0	214	26	W34506	Human anti-RSV monocl 3.52e+00
39	63	100.0	234	21	W11638	Humanised light chain 3.52e+00
40	63	100.0	235	29	W41411	Humanised antibody 80 3.52e+00
41	63	100.0	235	29	W41398	Human anti-RSV monocl 3.52e+00
42	63	100.0	235	21	W11640	Chimeric humanised Mu 3.52e+00
43	63	100.0	240	29	W23954	Humanised anti-CD38 m 3.52e+00
44	63	100.0	245	19	R98943	Humanised anti-CD38 m 3.52e+00
45	63	100.0	355	28	W35133	R. papiens recombinan 3.52e+00

ALIGNMENTS

RESULT 1
 ID W52225; standard: Protein; 104 AA.
 AC W52225;
 DE 12-JUN-1998 (first entry)
 DF Antibody LD2-4-VL chain sequence.
 DE Antibody; variable heavy chain; VH chain; variable light chain; VL chain;
 KW Rhesus D antigen; anti-Rhesus D immunoglobulin; HDN; therapy;
 KM Idiopathic thrombocytopenic purpura; haemolytic disease of the newborn.
 OS Homo sapiens.
 PN W09749809-A1.
 PD 31-DEC-1997.
 PE 20-JUN-1997; E03253.
 PF 20-JUN-1996; EP-810421.
 PR (ROTK-) ROTKREUTZSTIFUNG ZENT LAB BLUTSPENDE.
 PA Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
 PI Vogel M;
 DR WPI; 98-077173/07.
 DR N-PSDB: V19749.
 PT New Rhesus D antigen binding polypeptide(s) - used to neutralise
 PT Rhesus D antigen in therapy, e.g. for treating idiopathic
 PT thrombocytopenic purpura.
 PS Claim 1; Fig 7B; 68pp; English.
 CC This sequence is the antibody LD2-4-VL chain sequence, which is a
 CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rhesus D antigens which
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rhesus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rhesus negative women before or immediately after the birth
 CC of a Rhesus positive child to prevent haemolytic disease of the newborn
 CC (HDN) in subsequent pregnancies. In addition, anti-Rhesus D
 CC immunoglobulin can be used after transfusions of Rhesus positive blood
 CC to Rhesus negative recipients in order to prevent sensitisation to the
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.
 CC Sequence 104 AA:
 Query Match 100.0%; Score 63; DB 29; Length 104;
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PD 31-DEC-1997. E03253.
 PF 20-JUN-1997; EP-810421.
 PR 24-JUN-1996; EP-810421.
 PA (ROK-) ROTKREUZSTIFTUNG ZENT LAB BLUTSPENDE.
 PI Amstutz H, Imboden M, Miescher S, Morell A, Stadler B,
 PI Vogel M;
 DR WPI: 98-077173/07.
 DR N-PSDB; V19745.
 PT New Rhesus D antigen binding polypeptide(s) - used to neutralise
 PT Rhesus D antigen in therapy, e.g. for treating idiopathic
 PT thrombocytopenic purpura
 PS Claim 1; Fig 5B; 68pp; English.
 CC This sequence is the antibody LDI-117-VL chain sequence, which is a
 CC polypeptide of the invention. The polypeptides are capable of forming
 CC antigen binding structures with specificity for Rhesus D antigens which
 CC include Rhesus D-specific CDR 1, CDR 2, and CDR 3 regions of pairs of
 CC variable heavy (VH) and variable light (VL) chain sequences. The
 CC antibodies are active against the Rhesus D antigen. They can be used for
 CC treating disorders which would benefit from anti-Rhesus D immunoglobulin,
 CC e.g. idiopathic thrombocytopenic purpura. They can also be used for the
 CC protection of Rhesus negative women before or immediately after the birth
 CC of a Rhesus positive child to prevent hemolytic disease of the newborn
 CC (HUN) in subsequent pregnancies. In addition, anti-Rhesus D
 CC immunoglobulin can be used after mistransfusions of Rhesus positive blood
 CC to Rhesus negative recipients in order to prevent sensitisation to the
 CC Rhesus D antigen. The products can also be used as diagnostic reagents.
 SO Sequence 106 AA;

Query Match 100.0%; Score 63; DB 29; Length 106;
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 mtgspsslsas 12
 |||||
 24 MTGSPSSLAS 34

RESULT 12
 ID W22412 standard; Protein; 106 AA.
 AC W22412;
 DT 08-DEC-1997 (first entry)
 DE Humanised alpha-4 integrin antibody 21.6 VL Ia.
 KW alpha-4 integrin; humanised antibody; monoclonal antibody 21.6;
 KW asthma; atherosclerosis; AIDS; dementia; diabetes; tumour;
 KW metastasis; inflammatory bowel disease; rheumatoid arthritis;
 KW transplant rejection; graft versus host disease; nephritis;
 KW atopic dermatitis; psoriasis; myocardial ischemia;
 KW acute leukocyte mediated lung injury; therapy.
 KW Chimeric Mus musculus;
 KW Chimeric Homo sapiens;
 CC Chimeric synthetic.
 FH Key
 FT location/Qualifiers
 FT 1..23
 FT region /label= FR1
 FT /note= "REI framework region 1"
 FT 24..34
 FT region /label= CDR1
 FT /note= "21.6 complementarity determining region 1"
 FT 35..49
 FT region /label= FR2
 FT /note= "REI framework region 2"
 FT misc-difference 45
 FT /note= "REI Lys-45 is subst. by Lys of mouse
 FT 21.6 VL, important in supporting the
 FT CDR2 loop"
 FT 49
 FT /note= "REI Tyr-49 is subst. by His of mouse
 FT 21.6 VL, located at the binding site"
 FT region /label= CDR2
 FT /note= "21.6 complementarity determining region 2"
 FT 57..88
 FT region /label= FR3

FT /note= "REI framework region 3"
 FT misc-difference 58
 FT /note= "REI Val-58 is subst. by Ile of mouse
 FT 21.6 VL, important in supporting the CDR2
 FT loop"
 FT misc-difference 69
 FT /note= "REI Thr-69 is subst. by Arg of mouse
 FT 21.6 VL, involved in antibody-antigen
 FT binding"
 FT 89..96
 FT region /label= CDR3
 FT /note= "21.6 complementarity determining region 3"
 FT 97..106
 FT /label= FR4
 FT /note= "REI framework region 4"
 FT misc-difference 103
 FT /note= "REI Leu-103 subst. by Val, more typical
 FT of human kappa light chain J region"
 FT misc-difference 104
 FT /note= "REI Gln-104 subst. by Glu, more typical
 FT of human kappa light chain J region"
 FT misc-difference 106
 FT /note= "REI Thr-106 subst. by Lys, more typical
 FT of human kappa light chain J region"
 FT PN W09718838-A1.
 PD 29-MAY-1997.
 PE 21-NOV-1996; U18807.
 PR 21-NOV-1995; US-561521.
 PA (ATHE-) ATHENA NEUROSCIENCES INC.
 PI Bondy KM, Jones ST, Leger OJ, Saldanha J, Yednock TA;
 DR WPI: 97-297879/27.
 PT Uses of humanised alpha-4 integrin antibody - for treatment of
 PT asthma, atherosclerosis, AIDS, dementia, etc.
 PS Claim 25; Fig 6; 107pp; English.
 CC This polypeptide, designated Ia, comprises the light chain variable
 CC region (VL) of a humanised alpha-4 integrin antibody 21.6. It is
 CC composed of complementarity determining regions (CDRs) from the VL
 CC region (see W22409) of mouse alpha-4 integrin monoclonal antibody
 CC 21.6 and a modified human REI framework. It can be expressed in
 CC mammalian host cells following PCR amplification and mutagenesis
 CC of appropriate fragments of mouse and human DNA sequences. The
 CC humanised 21.6 VL and a humanised 21.6 VH (see W22413) can be used
 CC to produce a claimed humanised 21.6 antibody that is useful in the
 CC manufacture of a medicament for treating asthma, atherosclerosis,
 CC AIDS, dementia, diabetes, inflammatory bowel disease, rheumatoid
 CC arthritis, transplant rejection, graft versus host disease, tumour
 CC metastasis, nephritis, atopic dermatitis, psoriasis, myocardial
 CC ischemia, and acute leukocyte mediated lung injury. The antibody
 CC may also be used in the affinity purification of alpha-4 integrin
 CC for use as a vaccine or an immunogen. It is also useful for
 CC generating idiotypic antibodies. The humanised antibody has a
 CC half-life in the human circulation essentially equivalent to that
 CC of naturally occurring human antibodies.
 SO Sequence 106 AA;

Query Match 100.0%; Score 63; DB 24; Length 106;
 Best Local Similarity 100.0%; Pred. No. 3.52e+00;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 mtgspsslsas 14
 |||||
 24 MTGSPSSLAS 34

RESULT 13
 ID W41390 standard; Protein; 107 AA.
 AC W41390;
 DT 02-JUN-1998 (first entry)
 DE Anti-CEA antibody light chain variable region VK4.
 KW Anti-CEA antibody; carcinoembryonic antigen; 806.077 Ab; cancer therapy;
 KW cancer diagnosis; complementarity determining region; light chain.
 OS Synthetic.
 PN W09743329-A1.

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(TM)

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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
on: Tue Mar 23 15:20:39 1999; Maspar time 1.37 Seconds
Molecular output not generated. 34.477 Million cell updates/sec

Title: >US-08-766-350A-4
Description: (31-35) from US08766350A.pep (2 of 4)
Perfect Score: 31
Sequence: 1 VRSGA 5

Scoring table: PAM 150
Gap 11

Searched: 100342 seqs, 9469514 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfilest1

Statistics: Mean 11.797; Variance 23.980; scale 0.492

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Hit	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	31	100.0	124	2	US-08-471-	Sequence 6, Applicatio	1.86e+02	
2	31	100.0	124	1	US-08-017-	Sequence 4, Applicatio	1.86e+02	
3	31	100.0	124	2	US-08-471-	Sequence 4, Applicatio	1.86e+02	
4	31	100.0	124	3	PCT-US94-0	Sequence 6, Applicatio	1.86e+02	
5	31	100.0	124	1	US-08-017-	Sequence 6, Applicatio	1.86e+02	
6	31	100.0	124	3	PCT-US94-0	Sequence 4, Applicatio	1.86e+02	
7	31	100.0	221	2	US-08-342-	Sequence 5, Applicatio	1.86e+02	
8	31	100.0	341	1	US-08-314-	Sequence 19, Applicati	1.86e+02	
9	31	100.0	386	2	US-08-663-	Sequence 6, Applicatio	1.86e+02	
10	31	100.0	484	1	US-08-482-	Sequence 26, Applicati	1.86e+02	
11	31	100.0	484	1	US-08-127-	Sequence 26, Applicati	1.86e+02	
12	31	100.0	659	1	US-08-116-	Sequence 3, Applicatio	1.86e+02	
13	31	100.0	659	2	US-08-479-	Sequence 3, Applicatio	1.86e+02	
14	31	100.0	691	2	PCT-US91-0	Sequence 2, Applicatio	1.86e+02	
15	29	93.5	73	2	US-08-379-	Sequence 7, Applicatio	3.70e+02	
16	29	93.5	185	4	5514590-10	Patent No. 5514590.	3.70e+02	
17	29	93.5	185	1	US-08-278-	Sequence 14, Applicati	3.70e+02	
18	29	93.5	185	1	US-08-483-	Sequence 14, Applicati	3.70e+02	
19	29	93.5	185	1	US-08-472-	Sequence 14, Applicati	3.70e+02	
20	29	93.5	185	2	US-08-487-	Sequence 14, Applicati	3.70e+02	
21	29	93.5	299	4	5514590-4	Patent No. 5514590.	3.70e+02	
22	29	93.5	396	2	US-08-926-	Sequence 2, Applicatio	3.70e+02	
23	29	93.5	421	2	US-07-955-	Sequence 27, Applicati	3.70e+02	

24	29	93.5	471	3	PCT-US95-0	Sequence 2, Applicatio	3.70e+02
25	29	93.5 <td>516</td> <td>1<th>US-08-356-</th><th>Sequence 4, Applicatio</th><th>3.70e+02</th></td>	516	1 <th>US-08-356-</th> <th>Sequence 4, Applicatio</th> <th>3.70e+02</th>	US-08-356-	Sequence 4, Applicatio	3.70e+02
26	29	93.5 <td>559</td> <td>2<th>US-08-661-</th><th>Sequence 16, Applicati</th><th>3.70e+02</th></td>	559	2 <th>US-08-661-</th> <th>Sequence 16, Applicati</th> <th>3.70e+02</th>	US-08-661-	Sequence 16, Applicati	3.70e+02
27	29	93.5 <td>559</td> <td>1<th>US-08-406-</th><th>Sequence 20, Applicati</th><th>3.70e+02</th></td>	559	1 <th>US-08-406-</th> <th>Sequence 20, Applicati</th> <th>3.70e+02</th>	US-08-406-	Sequence 20, Applicati	3.70e+02
28	29	93.5 <td>1018</td> <td>1<th>US-08-714-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1018	1 <th>US-08-714-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-08-714-	Sequence 6, Applicatio	3.70e+02
29	29	93.5 <td>1018</td> <td>1<th>US-08-452-</th><th>Sequence 2, Applicatio</th><th>3.70e+02</th></td>	1018	1 <th>US-08-452-</th> <th>Sequence 2, Applicatio</th> <th>3.70e+02</th>	US-08-452-	Sequence 2, Applicatio	3.70e+02
30	29	93.5 <td>1018</td> <td>1<th>US-08-408-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1018	1 <th>US-08-408-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-08-408-	Sequence 6, Applicatio	3.70e+02
31	29	93.5 <td>1018</td> <td>1<th>US-08-408-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1018	1 <th>US-08-408-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-08-408-	Sequence 6, Applicatio	3.70e+02
32	29	93.5 <td>1045</td> <td>1<th>US-07-783-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1045	1 <th>US-07-783-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-07-783-	Sequence 6, Applicatio	3.70e+02
33	29	93.5 <td>1045</td> <td>1<th>US-07-934-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1045	1 <th>US-07-934-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-07-934-	Sequence 6, Applicatio	3.70e+02
34	29	93.5 <td>1045</td> <td>1<th>US-07-596-</th><th>Sequence 6, Applicatio</th><th>3.70e+02</th></td>	1045	1 <th>US-07-596-</th> <th>Sequence 6, Applicatio</th> <th>3.70e+02</th>	US-07-596-	Sequence 6, Applicatio	3.70e+02
35	28	90.3 <td>275</td> <td>4<th>5472855-4</th><th>Patent No. 5472855.</th><th>5.19e+02</th></td>	275	4 <th>5472855-4</th> <th>Patent No. 5472855.</th> <th>5.19e+02</th>	5472855-4	Patent No. 5472855.	5.19e+02
36	28	90.3 <td>380</td> <td>4<th>RE34606-2</th><th>Patent No. RE34,606.</th><th>5.19e+02</th></td>	380	4 <th>RE34606-2</th> <th>Patent No. RE34,606.</th> <th>5.19e+02</th>	RE34606-2	Patent No. RE34,606.	5.19e+02
37	28	90.3 <td>616</td> <td>2<th>US-08-638-</th><th>Sequence 35, Applicati</th><th>5.19e+02</th></td>	616	2 <th>US-08-638-</th> <th>Sequence 35, Applicati</th> <th>5.19e+02</th>	US-08-638-	Sequence 35, Applicati	5.19e+02
38	28	90.3 <td>774</td> <td>1<th>US-07-747-</th><th>Sequence 3, Applicatio</th><th>5.19e+02</th></td>	774	1 <th>US-07-747-</th> <th>Sequence 3, Applicatio</th> <th>5.19e+02</th>	US-07-747-	Sequence 3, Applicatio	5.19e+02
39	28	90.3 <td>774</td> <td>1<th>US-08-019-</th><th>Sequence 5, Applicatio</th><th>5.19e+02</th></td>	774	1 <th>US-08-019-</th> <th>Sequence 5, Applicatio</th> <th>5.19e+02</th>	US-08-019-	Sequence 5, Applicatio	5.19e+02
40	28	90.3 <td>780</td> <td>2<th>US-08-786-</th><th>Sequence 14, Applicati</th><th>5.19e+02</th></td>	780	2 <th>US-08-786-</th> <th>Sequence 14, Applicati</th> <th>5.19e+02</th>	US-08-786-	Sequence 14, Applicati	5.19e+02
41	28	90.3 <td>853</td> <td>2<th>US-08-638-</th><th>Sequence 27, Applicati</th><th>5.19e+02</th></td>	853	2 <th>US-08-638-</th> <th>Sequence 27, Applicati</th> <th>5.19e+02</th>	US-08-638-	Sequence 27, Applicati	5.19e+02
42	28	90.3 <td>853</td> <td>2<th>US-08-638-</th><th>Sequence 31, Applicati</th><th>5.19e+02</th></td>	853	2 <th>US-08-638-</th> <th>Sequence 31, Applicati</th> <th>5.19e+02</th>	US-08-638-	Sequence 31, Applicati	5.19e+02
43	28	90.3 <td>1958</td> <td>1<th>US-07-945-</th><th>Sequence 2, Applicatio</th><th>5.19e+02</th></td>	1958	1 <th>US-07-945-</th> <th>Sequence 2, Applicatio</th> <th>5.19e+02</th>	US-07-945-	Sequence 2, Applicatio	5.19e+02
44	28	90.3 <td>2842</td> <td>1<th>US-08-289-</th><th>Sequence 2, Applicatio</th><th>5.19e+02</th></td>	2842	1 <th>US-08-289-</th> <th>Sequence 2, Applicatio</th> <th>5.19e+02</th>	US-08-289-	Sequence 2, Applicatio	5.19e+02
45	28	90.3 <td>2873</td> <td>2<th>US-08-638-</th><th>Sequence 2, Applicatio</th><th>5.19e+02</th></td>	2873	2 <th>US-08-638-</th> <th>Sequence 2, Applicatio</th> <th>5.19e+02</th>	US-08-638-	Sequence 2, Applicatio	5.19e+02

ALIGNMENTS

RESULT 1 STANDARD; PRT; 124 AA.

US-08-471-426-6

xxxxxx

Sequence 6, Application US/08471426

Sequence 6, Application US/08471426

Patent No. 5808033

GENERAL INFORMATION:

APPLICANT: GOURLIE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: MEZES, PETER S

APPLICANT: KAPLAN, DONALD A

APPLICANT: SCHLOM, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Duane C. Ulmer

STREET: P.O. Box 1967

CITY: Midland

STATE: MI

COUNTRY: US

ZIP: 48641-1967

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,426

FILING DATE: 06-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/017,570

FILING DATE: 16-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: ULMER, DUANE C

REGISTRATION NUMBER: 34,941

REFERENCE/DOCKET NUMBER: C-38,777

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

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CC LENGTH: 124 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 124 AA; 13816 MW; 93186 CN;

Query Match 100.0%; Score 31; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.86e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 VRSGA 16
|
|
|
|
OY 31 VRSGA 35

RESULT 2
ID US-08-017-570-4 STANDARD: PRT; 124 AA.
xxxxxx

Sequence 4, Application US/08017570

Sequence 4, Application US/08017570
Patent No. 5472693

GENERAL INFORMATION:

APPLICANT: GOURLIE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: MEZES, PETER S

APPLICANT: KAPLAN, DONALD A

APPLICANT: SCHLOM, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Duane C. Ulmer

STREET: P.O. Box 1967

CITY: Midland

STATE: MI

COUNTRY: US

ZIP: 48641-1967

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/017,570

FILING DATE: 19930216

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: ULMER, DUANE C

REGISTRATION NUMBER: 34,941

REFERENCE/DOCKET NUMBER: C-38,777

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 124 AA; 13786 MW; 91250 CN;

Query Match 100.0%; Score 31; DB 1; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.86e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
ID US-08-471-426-4 STANDARD: PRT; 124 AA.
xxxxxx

Sequence 4, Application US/08471426

Sequence 4, Application US/08471426
Patent No. 5808033

GENERAL INFORMATION:

APPLICANT: GOURLIE, BRIAN B

APPLICANT: RIXON, MARK W

APPLICANT: MEZES, PETER S

APPLICANT: KAPLAN, DONALD A

APPLICANT: SCHLOM, JEFFREY

TITLE OF INVENTION: A NOVEL FAMILY OF ANTI-CARCINOEMBRYONIC

TITLE OF INVENTION: ANTIGEN CHIMERIC ANTIBODIES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Duane C. Ulmer

STREET: P.O. Box 1967

CITY: Midland

STATE: MI

COUNTRY: US

ZIP: 48641-1967

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/471,426

FILING DATE: 06-JUN-1995

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/017,570

FILING DATE: 16-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: ULMER, DUANE C

REGISTRATION NUMBER: 34,941

REFERENCE/DOCKET NUMBER: C-38,777

TELECOMMUNICATION INFORMATION:

TELEPHONE: (517) 636-8104

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 124 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 124 AA; 13786 MW; 91250 CN;

Query Match 100.0%; Score 31; DB 2; Length 124;
Best Local Similarity 100.0%; Pred. No. 1.86e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 12 VRSGA 16
|
|
|
|
OY 31 VRSGA 35

RESULT 4
ID PCT-US94-01709-6 STANDARD: PRT; 124 AA.
xxxxxx

Sequence 6, Application PC/TUS9401709

Sequence 6, Application PC/TUS9401709

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